

A17N: Ed Hart

Access DB#

12/499

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

Requester's Full Name Celine Pisan Examiner # 78710 Date 5/6/04
Air Unit 1636 Phone Number 2-0777 Serial Number 101009445
Mail Box and Bldg Room Location 2A 37 Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention OX 2 Receptor Homologs

Inventors (please provide full names): Barclay et al.

Earliest Priority Filing Date 5/13/1999

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search, SEQ ID NO: 20 - AA-348

MEJ

STAFF USE ONLY

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone: _____	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Quester, Orbit _____
Pat. Assignment: <u>5/27/04</u>	Bibliographic _____	Orbit _____
Date Completed: <u>5/27/04</u>	Citation _____	Lexis Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>ESP</u>
Client Prep Time: _____	Patent Family _____	WWW Internet _____
Indexing Time: _____	Other _____	Other vendors _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 121499

TO: Celine Qian
Location: rem/2a89/2c70
Art Unit: 1636
Friday, May 07, 2004

Case Serial Number: 10/009445

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC SEARCH RESULT FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 11:33:09 ; Search time 60 Seconds
(without alignments)
1638.776 Million cell updates/sec

Title: US-10-009-445a-20

Perfect score: 1846
Sequence: 1 MLCFMTATNGLLILITFL.....NKVKASQALQSEVDLHTL 348

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1846	100.0	348	4 AAB48016	AB48016 Human OX2
2	1846	100.0	348	5 AEG91409	ABG91409 Primate L
3	1846	100.0	348	6 ABB82703	ABB82703 Human OX2
4	1843	99.8	348	4 AAU29270	AAU29270 Human PRO
5	1843	99.8	348	6 ABUS8646	ABUS8646 Human PRO
6	1843	99.8	348	6 ABUS8194	ABUS8194 Novel hum
7	1843	99.8	348	6 ABUS84509	ABUS84509 Human sec
8	1843	99.8	348	6 ABR66383	ABR66383 Human sec
9	1843	99.8	348	6 ABR65773	ABR65773 Human sec
10	1843	99.8	348	6 ABUS9713	ABUS9713 Human sec
11	1843	99.8	348	6 ABUS2952	ABUS2952 Human PRO
12	1843	99.8	348	6 ABUS9073	ABUS9073 Human hum
13	1843	99.8	348	6 ABR68322	ABR68322 Human hum
14	1843	99.8	348	6 ABUS6375	ABUS6375 Novel hum
15	1843	99.8	348	6 ABUS92806	ABUS92806 Human sec
16	1843	99.8	348	6 ABR02883	ABR02883 Human sec
17	1843	99.8	348	6 ABR02835	ABR02835 Human sec
18	1843	99.8	348	6 ABR75089	ABR75089 Human sec
19	1843	99.8	348	6 ABR94851	ABR94851 Human sec
20	1843	99.8	348	6 ABUS8524	ABUS8524 Human PRO
21	1843	99.8	348	6 ABUS98984	ABUS98984 Novel hum
22	1843	99.8	348	6 ABUS9199	ABUS9199 Novel hum
23	1843	99.8	348	6 ABUS1905	ABUS1905 Novel hum
24	1843	99.8	348	6 ABUS9598	ABUS9598 Human PRO
25	1843	99.8	348	6 ABUS6439	ABUS6439 Human sec

25	1843	99.8	348	6 ABUS67652	ABUS67652 Human sec
27	1843	99.8	348	6 ABUS0680	ABUS0680 Human PRO
28	1843	99.8	348	6 ABR9598	ABR9598 Human sec
29	1843	99.8	348	6 ABR98988	ABR98988 Human sec
30	1843	99.8	348	6 ABR016511	ABR016511 Human sec
31	1843	99.8	348	6 ABR92411	ABR92411 Human sec
32	1843	99.8	348	6 ABR019052	ABR019052 Human sec
33	1843	99.8	348	6 ABR78473	ABR78473 Human sec
34	1843	99.8	348	6 ABUS85209	ABUS85209 Novel hum
35	1843	99.8	348	6 ABR000348	ABR000348 Novel hum
36	1843	99.8	348	6 ABR011680	ABR011680 Human sec
37	1843	99.8	348	6 ABR002325	ABR002325 Human sec
38	1843	99.8	348	6 ABUS8899	ABUS8899 Novel hum
39	1843	99.8	348	6 ABUS3594	ABUS3594 Human sec
40	1843	99.8	348	6 ABR06395	ABR06395 Novel hum
41	1843	99.8	348	6 ABR59431	ABR59431 Human sec
42	1843	99.8	348	6 ABR009493	ABR009493 Human sec
43	1843	99.8	348	6 ABR019357	ABR019357 Novel hum
44	1843	99.8	348	6 ABR011375	ABR011375 Human sec
45	1843	99.8	348	6 ABR66993	ABR66993 Human sec

ALIGNMENTS

RESULT 1	AB48016	AB48016 standard; protein; 348 AA.
XX	XX	XX
AC	AB48016;	
DT	19-MAR-2001 (first entry)	
DE	Human OX2R homologue 1.2 (OX2RH1.2) polypeptide sequence.	
XX	XX	XX
XX	OX2R protein; OX2RH1; OX2RH2; OX2RH3; OX2RH4; OX2RH1.2; ischaemia;	
KW	antiinflammatory; cytoprotective; neuroprotective; nociceptive; human;	
KW	antiartherosclerotic; vasodilator; immunosuppressive; antithrombotic;	
XX	antitumor; gene therapy.	
OS	Homo sapiens.	
XX	XX	XX
FT	Key	Location/Qualifiers
FT	Reptide	1..25
FT	Protein	/note="signal peptide"
FT	FT	26..348
XX	XX	/note="mature protein"
XX	XX	XX
PN	MO200070045-A1.	
XX	XX	XX
PD	23-NOV-2000.	
XX	XX	XX
PF	11-MAY-2000; 2000MO-US012998.	
XX	XX	XX
PR	13-MAY-1999; 99GB-00011123.	
PR	03-NOV-1999; 99GB-00025989.	
PA	(MED1-) MEDICAL RES COUNCIL.	
XX	(SCHE) SCHERING CORP.	
PI	Barclay AN, Brown WH, Gorman DM, Lantier LL, Wright GJ;	
PI	Cherlyne H, Phillips JH, Hoek RW, Sedgwick JD;	
DR	WPI; 2001-016233/02.	
DR	N-PSDB; AAC84177, AAC84178.	
XX	XX	XX
PT	Mammalian OX2R proteins and DNA sequences useful for modulating the	
PT	physiology and development of a cell.	
XX	XX	XX
PS	Claim 1; Page 25-26; 142PP; English.	
XX	XX	XX
CC	The invention relates to rodent or primate OX2R proteins, especially	
CC	OX2RH1, OX2RH2, OX2RH3, OX2RH4, or OX2RH1.2 proteins. Agonists and	

CC antagonists of the OX2R sequences can be used to modulate physiology or
 CC development of a cell, particularly for enhancing myeloid function or
 CC enhancing immunity. The sequences can be used to identify non-OX2 ligands
 CC for an OX2R. The polypeptides and polynucleotides can be used to treat
 CC inflammatory, leukoproliferative and neurodegenerative or post-traumatic
 CC conditions, including atherosclerosis, multiple sclerosis, ischemia,
 CC neurodegeneration, rheumatoid arthritis, and autoimmunity. The present
 CC sequence represents the human OX2R homologue 1.2 (OX2RH1.2) polypeptide
 XX
 SQ Sequence 348 AA;

Query Match 100.0%; Score 1846; DB 4; Length 348;
 Best Local Similarity 100.0%; Pred. No. 2.3e-169;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLIIITIFVAEAGAAPNNLSIMQTSKXENHALASSSLCMEDEKQITON 60
 DB 1 MLCPRRTANLGLLIIITIFVAEAGAAPNNLSIMQTSKXENHALASSSLCMEDEKQITON 60
 QY 61 YSKVLAEVNTSWPVKATNAVLCCEPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 DB 61 YSKVLAEVNTSWPVKATNAVLCCEPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 QY 121 TNCDEBITWSPRPDQNSDLQIRPVAITHDGYRCIMWTPDGNFRHGYHLOVLTPEVTL 180
 DB 121 TNCDEBITWSPRPDQNSDLQIRPVAITHDGYRCIMWTPDGNFRHGYHLOVLTPEVTL 180
 QY 181 FQNRNRTAVCKAVAGKRAQISWIPGDCATKQEYWSNGTVKSTCHMEVNAVSTVTC 240
 DB 181 FQNRNRTAVCKAVAGKRAQISWIPGDCATKQEYWSNGTVKSTCHMEVNAVSTVTC 240
 QY 241 VSHLTGKNSLYIELLPVPGAKKSATLYPIYIIITLITVGFIMLVKNGCRKYKLNKT 300
 DB 241 VSHLTGKNSLYIELLPVPGAKKSATLYPIYIIITLITVGFIMLVKNGCRKYKLNKT 300
 QY 301 ESTPVEEDEMOPYASYTEKNPLVDITNKVKAQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPYASYTEKNPLVDITNKVKAQALQSEVDTDLHTL 348

RESULT 2
 ABG91409
 ID ABG91409 standard; protein; 348 AA.

AC ABG91409;

DT 29-NOV-2002 (first entry)

DE Primate LP209.

XX Primate; LP194; LP263a; LP263b; LP264; LP265; LP283; LP286; LP284; LP282;
 XX LP273; LP277; LP287; LP209; LP209c; LP209d; LP293; LP294; LP295;
 XX cell proliferative disorder; actinic keratosis; arteriosclerosis;
 XX burster's; hepatitis; cancer; autoimmune disorder; inflammatory disorder;
 XX acquired immune deficiency syndrome; AIDS; asthma; anaemia; allergy;
 XX atopic dermatitis; cardiovascular; ischaemic heart disease; tumour;
 XX neurological; epilepsy; stroke; Alzheimer's disease; developmental.

OS Mammalia.

PN WO200263009-A2.

PD 15-AUG-2002.

PF 28-JAN-2002; 2002WO-US000525.

PR 02-FEB-2001; 2001US-0266359P.

PR 21-FEB-2001; 2001US-0270564P.

PR 13-JUL-2001; 2001US-0305058P.

XX (ELIL) LILLY & CO ELI.
 XX Bhattacharya, Calley JN, Heuer JG, Kelenher GP, Lancaster JS, Li Q;

PI Lu D, Mills EJ, Mishra SK, Perkins DR, Rowlinson SW, Smith RC;
 PI Su EW, Wang H, Zhi Y;
 XX WPI; 2002-643415/69.
 DR N-PSDB; AB867725.
 XX New mammalian LP proteins and nucleic acids useful in diagnosing,
 XX treating and preventing cell proliferative, autoimmune/inflammatory,
 XX cardiovascular, neurological, and developmental disorders.
 PS Claim 13; Page 50; 277pp; English.

XX The invention relates to an isolated or recombinant polynucleotide (I)
 CC comprising a mature coding portion of LP194, LP263a, LP263b, LP264,
 CC LP265, LP283, LP286, LP273, LP277, LP287, LP209, LP209b,
 CC LP209c, LP209d, LP293, LP294, or LP295; (I) is useful in diagnosing,
 CC treating, and preventing cell proliferative (e.g. actinic keratosis,
 CC arteriosclerosis, burster's, hepatitis or cancer), autoimmune/inflammatory
 CC (e.g. acquired immune deficiency syndrome (AIDS), asthma, anaemia,
 CC allergies or atopic dermatitis), cardiovascular (e.g. congestive heart
 CC failure, ischaemic heart disease, myocardial infarction, hypertensive
 CC heart disease, or vascular tumours), neurological (e.g. epilepsy, stroke,
 CC cerebral neoplasms, or Alzheimer's disease), and developmental (e.g.
 CC renal tubular acidosis, Cushing's syndrome, Duchenne and Becker muscular
 CC dystrophy, or hypothyroidism) disorders. These may also be used in
 CC assessing the effects of exogenous compounds on the expression of nucleic
 CC acid and amino acid sequences of such proteins, and in chromosome
 CC identification. The proteins are further used in generating antibody that
 CC specifically and/or selectively binds an LP protein. ABG91397-ABG91415
 CC represent primate LP protein sequences of the invention
 XX

SQ Sequence 348 AA;

Query Match 100.0%; Score 1846; DB 5; Length 348;
 Best Local Similarity 100.0%; Pred. No. 2.3e-169;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLIIITIFVAEAGAAPNNLSIMQTSKXENHALASSSLCMEDEKQITON 60
 DB 1 MLCPRRTANLGLLIIITIFVAEAGAAPNNLSIMQTSKXENHALASSSLCMEDEKQITON 60
 QY 61 YSKVLAEVNTSWPVKATNAVLCCEPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 DB 61 YSKVLAEVNTSWPVKATNAVLCCEPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 QY 121 TNCDEBITWSPRPDQNSDLQIRPVAITHDGYRCIMWTPDGNFRHGYHLOVLTPEVTL 180
 DB 121 TNCDEBITWSPRPDQNSDLQIRPVAITHDGYRCIMWTPDGNFRHGYHLOVLTPEVTL 180
 QY 181 FQNRNRTAVCKAVAGKRAQISWIPGDCATKQEYWSNGTVKSTCHMEVNAVSTVTC 240
 DB 181 FQNRNRTAVCKAVAGKRAQISWIPGDCATKQEYWSNGTVKSTCHMEVNAVSTVTC 240
 QY 241 VSHLTGKNSLYIELLPVPGAKKSATLYPIYIIITLITVGFIMLVKNGCRKYKLNKT 300
 DB 241 VSHLTGKNSLYIELLPVPGAKKSATLYPIYIIITLITVGFIMLVKNGCRKYKLNKT 300
 QY 301 ESTPVEEDEMOPYASYTEKNPLVDITNKVKAQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPYASYTEKNPLVDITNKVKAQALQSEVDTDLHTL 348

RESULT 3
 ABB82703
 ID ABB82703 standard; protein; 348 AA.

AC ABB82703;

DT 07-MAR-2003 (first entry)

DE Human OX2R/CD200R full-length (FL) protein.

XX OX2; OX2 receptor; OX2R; transmembrane protein; CD200; CD200R; human;
 XX

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.

PS Claim 11; Fig 494; 774pp; English.

CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumor in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumor in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumor necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumors and also
CC susceptibility to tumor development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumors, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders

SQ Sequence 348 AA:

Query Match 99.8%; Score 1843; DB 4; Length 348;
Best Local Similarity 99.7%; Pred. No. 4.5e-169;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCOPRTALVGLLITITFLVAVAGAGAPNNLSLMTSKENHALLASSLDCDEKQIION 60
DB 1 MCOPRTALVGLLITITFLVAVAGAGAPNNLSLMTSKENHALLASSLDCDEKQIION 60
QY 61 YSKVLAENVTSVPVKATNAVLCCPEIALRNLIITWEILLNGQSCITKAYKETNETKE 120
DB 61 YSKVLAENVTSVPVKATNAVLCCPEIALRNLIITWEILLNGQSCITKAYKETNETKE 120
QY 121 TNCBTRITVWSPRPNQNSLOTRPAVITHDGYRCMTWPDNFRGHLOVLTPEVTL 180
DB 121 TNCBTRITVWSPRPNQNSLOTRPAVITHDGYRCMTWPDNFRGHLOVLTPEVTL 180
QY 181 FQNRNATVAVKAGRAQIAQISWIPEDCATKQEWNSNGTVKSTCHNEVANSVTCH 240
DB 181 FQNRNATVAVKAGRAQIAQISWIPEDCATKQEWNSNGTVKSTCHNEVANSVTCH 240
QY 241 VSHLTGNKSLYIELLVPGAKKSAKLYIYIITLITVGFIMLKNGCRKTKLNT 300
DB 241 VSHLTGNKSLYIELLVPGAKKSAKLYIYIITLITVGFIMLKNGCRKTKLNT 300
QY 301 ESTPVVEEDEMQPYASYTEKNPNFLVDTNKKVAKASQALQSEVDVDTLHTL 348
DB 301 ESTPVVEEDEMQPYASYTEKNPNFLVDTNKKVAKASQALQSEVDVDTLHTL 348

RESULT 5
ABU58646
ID ABU58646 standard; protein; 348 AA.

XX ABU58646;

XX 15-APR-2003 (first entry)

XX Human PRO polypeptide #247.

XX Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;

XX dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;

XX antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027272-A1.

PD 06-FEB-2003.
XX 21-JUN-2002; 2002US-00176492.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063540P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063730P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066120P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066772P.
XX 11-DEC-1997; 97US-0069335P.
XX 12-DEC-1997; 97US-0069425P.
XX 17-DEC-1997; 97US-0069870P.
XX 18-DEC-1997; 97US-0068017P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077649P.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078839P.
XX 27-MAR-1998; 98US-0079664P.
XX 27-MAR-1998; 98US-0079786P.
XX 31-MAR-1998; 98US-0080107P.
XX 31-MAR-1998; 98US-0080194P.
XX 01-APR-1998; 98US-0080327P.
XX 01-APR-1998; 98US-0080333P.
XX 08-APR-1998; 98US-0081049P.
XX 08-APR-1998; 98US-0081070P.
XX 09-APR-1998; 98US-0081195P.
XX 15-APR-1998; 98US-0081838P.
XX 21-APR-1998; 98US-0082568P.
XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082797P.
XX 28-APR-1998; 98US-0083322P.
XX 29-APR-1998; 98US-0083495P.
XX 29-APR-1998; 98US-0083496P.
XX 29-APR-1998; 98US-0083498P.
XX 29-APR-1998; 98US-0083499P.
XX 05-MAY-1998; 98US-0084366P.
XX 06-MAY-1998; 98US-0084414P.
XX 07-MAY-1998; 98US-0084639P.
XX 07-MAY-1998; 98US-0084640P.
XX 07-MAY-1998; 98US-0084643P.
XX 15-MAY-1998; 98US-0085579P.
XX 15-MAY-1998; 98US-0085600P.
XX 15-MAY-1998; 98US-0085680P.
XX 15-MAY-1998; 98US-0085700P.
XX 18-MAY-1998; 98US-0086032P.
XX 22-MAY-1998; 98US-0086392P.
XX 22-MAY-1998; 98US-0086486P.
XX 26-MAY-1998; 98US-0087098P.
XX 26-MAY-1998; 98US-0087208P.
XX 28-MAY-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088722P.
 PR 10-JUN-1998; 98US-0088728P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089090P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
 PR 22-JUN-1998; 98US-0090254P.
 PR 24-JUN-1998; 98US-0090429P.
 PR 24-JUN-1998; 98US-0090435P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 24-JUN-1998; 98US-0090461P.
 PR 24-JUN-1998; 98US-0090535P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090690P.
 PR 25-JUN-1998; 98US-0090694P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-00905413.
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 PR 26-AUG-1998; 98US-0098014P.
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 PR 15-SEP-1998; 98US-0100388P.
 PR 16-SEP-1998; 98US-0100622P.
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 PR 16-SEP-1998; 98US-0101751P.
 PR 16-SEP-1998; 98US-0101933P.
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 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-00168978.

Query Match 99.8%; Score 1843; DB 6; Length 348;
 Best Local Similarity 99.7%; Pred. No. 4,5e-169;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLILITFLVFAEAGAAQPNNSIMLQTSKENHAIASSSLCMEDEKQITON 60
 DB 1 MLCPRRTANLGLILITFLVFAEAGAAQPNNSIMLQTSKENHAIASSSLCMEDEKQITON 60
 QY 61 YSKVLAENVTSMPVMAANAVALCCPILARNLIIITWELIIIRGQSCTKAYRKENETKE 120
 DB 61 YSKVLAENVTSMPVMAANAVALCCPILARNLIIITWELIIIRGQSCTKAYRKENETKE 120
 QY 121 TNCEDERTITWVRPQNSDLQIRPAVATHDGYRCIMWTPDGNFRGHLQVLTPEVTL 180
 DB 121 TNCEDERTITWVRPQNSDLQIRPAVATHDGYRCIMWTPDGNFRGHLQVLTPEVTL 180
 QY 161 FQNRRTAVCAVAKVAKPAQAQISWIEGCAITQOEYWSNGTIVKSTCMEYHNVSTVCH 240
 DB 161 FQNRRTAVCAVAKVAKPAQAQISWIEGCAITQOEYWSNGTIVKSTCMEYHNVSTVCH 240
 QY 241 VSHLTGNSLYTELLPVGAKKSAKLIPYIIITIIITVGFIMLKVNGCRKYLKNT 300
 DB 241 VSHLTGNSLYTELLPVGAKKSAKLIPYIIITIIITVGFIMLKVNGCRKYLKNT 300
 QY 301 ESTPVEEDEMOPVASYTEKKNPLVDITNKVKAQALQSEVDITLHTL 348
 DB 301 ESTPVEEDEMOPVASYTEKKNPLVDITNKVKAQALQSEVDITLHTL 348

RESULT 6
 AB088194
 ID AB088194 standard, protein, 348 AA.
 XX
 AC AB088194;

XX 07-JUL-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO6015.
DE
XX Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
OS Homo sapiens.
XX
XX US200302127-A1.
XX
XX 13-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183012.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059263P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 28-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 11-DEC-1997; 97US-0066712P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
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PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
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PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
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PR 01-APR-1998; 98US-0080333P.
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PR 22-APR-1998; 98US-0082797P.
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PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
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PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
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PR 09-JUN-1998; 98US-0088655P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
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PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091632P.
PR 02-JUL-1998; 98US-0094006P.
PR 24-JUL-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095988P.
PR 10-AUG-1998; 98US-0096012P.
PR 10-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096897P.

PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 26-AUG-1998; 98US-0097952P.
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 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 01-SEP-1998; 98US-0098014P.
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 02-SEP-1998; 98US-0098803P.
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 PR 09-SEP-1998; 98US-0099602P.
 PR 10-SEP-1998; 98US-0099741P.
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 PR 10-SEP-1998; 98US-0099763P.
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 PR 16-SEP-1998; 98US-0100662P.
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 PR 29-SEP-1998; 98US-0102333P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.

Query Match 99.8%; Score 1843; DB 6; Length 348;
 Best Local Similarity 99.7%; Pred. No. 4.5e-169;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPPRTANTGLILITITFLVAEAGAQPNNISIMLQTSKENHALLASSSLCMDEKQITON 60
 DB 1 MLCPPRTANTGLILITITFLVAEAGAQPNNISIMLQTSKENHALLASSSLCMDEKQITON 60
 QY 61 YSKVLAENVTSWPMATNNAVLCCPFLAKNLIITWIIIRGQPSCTKAKRKETNTKE 120
 DB 61 YSKVLAENVTSWPMATNNAVLCCPFLAKNLIITWIIIRGQPSCTKAKRKETNTKE 120
 QY 121 TNCCTERTITWSPONSDLOIRPAVITHDGYRCIMWTPDGNFRAGYHLQVLVTPPEVTL 180
 DB 121 TNCCTERTITWSPONSDLOIRPAVITHDGYRCIMWTPDGNFRAGYHLQVLVTPPEVTL 180
 QY 181 FQNNRRTAVCAVAKPAAPAAQISWIPEDCATKQEWNSGTYTVASTCMEVHNASTVTC 240
 DB 181 FQNNRRTAVCAVAKPAAPAAQISWIPEDCATKQEWNSGTYTVASTCMEVHNASTVTC 240
 QY 241 VSHLTGNSLYIELLPVPGAKKSATLYPIYILITIIITVGFILWLKVNCGCRKXKLNKT 300

DB 241 VSHLTGNSLYIELLPVPGAKKSATLYPIYILITIIITVGFILWLKVNCGCRKXKLNKT 300
 QY 301 ESTPVEDEMQPYASTEKNNPLVDITNKYKASQALQSEVDTDLHTL 348
 DB 301 ESTPVEDEMQPYASTEKNNPLVDITNKYKASQALQSEVDTDLHTL 348

RESULT 7
 ABUS4509
 ID ABUS4509 standard; protein; 348 AA.
 XX
 AC ABUS4509;
 XX
 DT 02-AUG-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein (PRO) #247.
 XX
 KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
 KW tumour necrosis factor alpha; chondrocyte cell; tumour; Gene therapy;
 KW tissue typing.
 XX
 OS Homo sapiens.
 XX
 PN US2003032112-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 21-JUN-2002; 2002US-00176756.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 13-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 11-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0069670P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 20-MAR-1998; 98US-0078866P.
 PR 20-MAR-1998; 98US-0078839P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 31-MAR-1998; 98US-0080107P.
 PR 31-MAR-1998; 98US-0080194P.
 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080333P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 09-APR-1998; 98US-0081195P.
 PR 15-APR-1998; 98US-0081838P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 28-APR-1998; 98US-0083322P.
 PR 28-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.

QY 61 YSKYLAENVNTPYKMATNAVLCPPIALRRLIIITWEIIIRGQPSCTKAYRKEINETKE 120
Db 61 YSKYLAENVNTPYKMATNAVLCPPIALRRLIIITWEIIIRGQPSCTKAYRKEINETKE 120
QY 121 TNCYDERITWVSRPDQNSDQIRFVAITHDGYRCINWTPDGNFHRGYHLOVLTPEVTL 180
Db 121 TNCYDERITWVSRPDQNSDQIRFVAITHDGYRCINWTPDGNFHRGYHLOVLTPEVTL 180
QY 181 FQNNRFAVCAVGVKPAQISMTPEGDCATKQCYMANGVTVSTGCHWENHVSCTVCH 240
Db 181 FQNNRFAVCAVGVKPAQISMTPEGDCATKQCYMANGVTVSTGCHWENHVSCTVCH 240
QY 241 VSHLTGKSLYIELLPVPGAKSKAKLYIPYIIILITITVGPIMLKVNGCRKYLKNT 300
Db 241 VSHLTGKSLYIELLPVPGAKSKAKLYIPYIIILITITVGPIMLKVNGCRKYLKNT 300
QY 301 ESTVVEDEMOQPYASTYKKNPLDYTTNKVKSQALQSEYVDIDLTL 348
Db 301 ESTVVEDEMOQPYASTYKKNPLDYTTNKVKSQALQSEYVDIDLTL 348

RESULT 8
ABR66383
ID ABR66383 standard; protein, 348 AA.
XX ABR66383;
AC
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO6015, SEQ ID NO:494.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumor necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumor; diagnosis;
KW adrenal tumor; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antitumor; vulnerability; gene therapy.
XX
XX Homo sapiens.
XX OS
XX US2003027278-A1.
XX
XX
XX PD 06-FEB-2003.
XX
XX
XX 21-JUN-2002; 2002US-00176987.
XX
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 28-OCT-1997; 97US-0063540P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063734P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
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XX 12-DEC-1997; 97US-0068425P.
XX 17-DEC-1997; 97US-0069870P.
XX 18-DEC-1997; 97US-0068017P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077633P.
XX 11-MAR-1998; 98US-0077649P.
XX 20-MAR-1998; 98US-0078866P.
XX 20-MAR-1998; 98US-0078939P.

PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
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PR 15-MAY-1998; 98US-0085582P.
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 DB 61 YSKYLAENVTSWPKATNATVLCPPALRNLIITWELIIRQPSCTAYRRETEKTE 120
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 DB 121 TNCIDERITWSSRPDQNSDQIRPVAITHDGYRCIMVTPDGFHNGYHLQVLVTEVTL 180
 QY 181 FQNRRTAVCKAVAGKPAQISWIPGDCATKQETNSGTVYKSTCHMEVHNVSTYTC 240
 DB 181 FQNRRTAVCKAVAGKPAQISWIPGDCATKQETNSGTVYKSTCHMEVHNVSTYTC 240
 QY 241 VSHLTGKSLYIELLPYGAKKSAKIYPIIITLITLITVGFIMLKVNGCKRYLTKNT 300
 DB 241 VSHLTGKSLYIELLPYGAKKSAKIYPIIITLITLITVGFIMLKVNGCKRYLTKNT 300
 QY 301 ESTPVEEDMOPYASTEKNFLYDTNKKVKSQALQSEVDYDHTL 348
 DB 301 ESTPVEEDMOPYASTEKNFLYDTNKKVKSQALQSEVDYDHTL 348

RESULT 9
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 ID ABR65773 standard; protein; 348 AA.
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 AC ABR65773;
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 DT 05-AUG-2003 (first entry)
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 DE Human secreted polypeptide PRO6015, SEQ ID NO:494.
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 KW Human; PRO; secreted protein; transmembrane protein;
 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antithrombotic; vulnerable; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FN US2003036159-A1.
 XX
 PD 20-FEB-2003.
 XX
 FF 02-JUL-2002; 2002US-00186773.
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 DB 61 YSKVLAENVTSVPKATNAVACCPPIALRNLIITWEIILRGQSPCTKAYRKETNETKE 120
 QY 121 TNCQTERITWVSRPQNSDLOIRPVATHDGYRCIMTPQNGFRGHLOVLTPEVTL 180
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 DB 181 FQNRRTAVCAVAKVAGKPAQIAQIWIPEGDCATKQEWNSGTVVSKTCMEVHNVSTVCH 240
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 DB 241 VSHLGNKSLYELLPVPKAKSAYLYPIYIITITVGFIMLLKVNCGRKKLNKT 300
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RESULT 10
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 XX tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 XX tissue typing.
 OS Homo sapiens.
 XX
 PN US2003040070-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 27-JUN-2002; 2002US-00184627.
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Query Match 99.8%; Score 1843; DB 6; Length 348;
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QY 241 VSHLTGNKSLYIELLPVPGAKKSANKLYPIIITIIITIVGFIWLKNGCRKTKLNT 300
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DB 301 ESTPVVEDEMOQPYASYTEKNNPLVDITNKVKAQSLQSEVDTDLHTL 348

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RESULT 11
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XX AC ABU82952;
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XX DT
XX DE Human PRO polypeptide #247.
XX XX Human PRO polypeptide; secreted and transmembrane protein; tumour;
XX KM chromosome mapping; gene mapping; cytosolic.
XX XX

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DE Novel human secreted and transmembrane protein PRO6015.
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KW chondrocyte differentiation; tumour necrosis factor-alpha release;
KW affinity purification.
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OS Homo sapiens.
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PN US2003036147-A1.
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PE 02-JUL-2002; 2002US-00187741.
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PR 02-SEP-1998; 98US-0098803P.
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PR 02-SEP-1998; 98US-0098843P.
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PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
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PR 07-OCT-1998; 98US-00168978.

Query Match 99.8%; Score 1843; DB 6; Length 348;
Best Local Similarity 99.7%; Pred. No. 4,5e-169;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 181 FQNRRTAVCAKVAKPAQISWIEGDCATKQEWNSGTVKSTCHMEVHNVSTVTC 240
QY 241 VSHLTGNSLVIETLFPVGAKKSAKLYIPYILITITIVGFWLKNCGCKYKLNKT 300
DB 241 VSHLTGNSLVIETLFPVGAKKSAKLYIPYILITITIVGFWLKNCGCKYKLNKT 300
QY 301 ESTPVEDEDEMPYASYTEKNKPNLYDTTNKVKASQALQSEVDTDLHTL 348
DB 301 ESTPVEDEDEMPYASYTEKNKPNLYDTTNKVKASQALQSEVDTDLHTL 348

RESULT 13
ABR68322
ID ABR68322 standard; protein; 348 AA.
XX
AC ABR68322;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO6015, SEQ ID NO:494.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antitachytic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003027264-A1.
XX
PD 06-FEB-2003.
XX
PF 18-JUN-2002; 2002US-00174579.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
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 PR 26-AUG-1998; 98US-0097971P.
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 PR 01-SEP-1998; 98US-0098014P.
 PR 01-SEP-1998; 98US-0098716P.
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 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 13-SEP-1998; 98US-0099812P.
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 PR 18-SEP-1998; 98US-0100849P.
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 PR 25-SEP-1998; 98US-0101786P.
 PR 29-SEP-1998; 98US-0102207P.
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 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
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Query Match 99.8%; Score 1843; DB 6; Length 348;
 Best Local Similarity 99.7%; Pred. No. 4,56-169;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 MLCFWRITANIGLLIITLPIVAEAGAAQPNNSLMTQTSKFNALASSSICMDEKQITON 60
 Db 1 MLCFWRITANIGLLIITLPIVAEAGAAQPNNSLMTQTSKFNALASSSICMDEKQITON 60
 Cy 61 YSKYLAENVTSWPKVATNVALCCPPIALBNLIITWEIILRGQPSCTKAYRKEIETKE 120
 Db 61 YSKYLAENVTSWPKVATNVALCCPPIALBNLIITWEIILRGQPSCTKAYRKEIETKE 120
 Cy 121 TNCIDERITWSPRDQNSDQIQRPAITHDGYRCIMVTPDGNFNGYHLOVVTPEVTL 180
 Db 121 TNCIDERITWSPRDQNSDQIQRPAITHDGYRCIMVTPDGNFNGYHLOVVTPEVTL 180
 Cy 181 FQNRNRTAVCAKAGKPAQISWIPEDCATKQEYNSNGTVKSTCMWEHNVSTVTC 240
 Db 181 FQNRNRTAVCAKAGKPAQISWIPEDCATKQEYNSNGTVKSTCMWEHNVSTVTC 240
 Cy 241 VSHLTGNKSLYIELLPVPGAKKSAKIYPIIITIIITLVGFIWLTKNGCRTKLNKT 300
 Db 241 VSHLTGNKSLYIELLPVPGAKKSAKIYPIIITIIITLVGFIWLTKNGCRTKLNKT 300
 Cy 301 ESTPVEDEMDQPAAYSTEKNPNLYDTTNKVKASQALQSEVDIDHITL 348
 Db 301 ESTPVEDEMDQPAAYSTEKNPNLYDTTNKVKASQALQSEVDIDHITL 348

RESULT 14
 ABU96375
 ID ABU96375 standard; protein: 348 AA.
 ABU96375;
 25-JUL-2003 (first entry)
 DE Novel human secreted and transmembrane protein PRO6015.
 XX
 XX Human; secreted and transmembrane protein; PRO; transgenic animal;
 KW knockout; chromosome identification; tissue typing; tumour;
 KM chondrocyte proliferation; chondrocyte differentiation;
 KW tumor necrosis factor-alpha release stimulator.
 XX
 OS Homo sapiens.
 XX
 PN US2003036144-A1.
 PD 20-FEB-2003.
 XX
 PF 01-JUL-2002; 2002US-00187601.
 XX
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 31-OCT-1997; 97US-0065311P.
 PR 13-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0067122P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077643P.

PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102655P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.

Query Match 99.8%; Score 1843; DB 6; Length 348;
Best Local Similarity 99.7%; Pred. No. 4,5e-169;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRNTANIGLILITITFLVAEAGAAQPNNSLMQTSKENHALASSSLCWDKQIOTON 60
DB 1 MLCPRNTANIGLILITITFLVAEAGAAQPNNSLMQTSKENHALASSSLCWDKQIOTON 60
QY 61 YSKVLAENVTSWPKATNAVLCPPIALRNLIITWELLIGQPSCTKAYKKTNETKE 120
DB 61 YSKVLAENVTSWPKATNAVLCPPIALRNLIITWELLIGQPSCTKAYKKTNETKE 120
QY 121 TNCIDRITVSPDPQNSDIQIRPAVITHDGYRCIMVTPDGNFRGYYHLYLTPEVTL 180
DB 121 TNCIDRITVSPDPQNSDIQIRPAVITHDGYRCIMVTPDGNFRGYYHLYLTPEVTL 180
QY 181 FQNRNRTAVCKAVAGKPAQISWIPBGDCATKQEWNSGTWVTKSCHEVHNVSTVICH 240
DB 181 FQNRNRTAVCKAVAGKPAQISWIPBGDCATKQEWNSGTWVTKSCHEVHNVSTVICH 240
QY 241 VSHLTGNKSLYITLLPVPKAKSAKLYPIYIIITIIITVGYIMLKNGCRKTKLNT 300
DB 241 VSHLTGNKSLYITLLPVPKAKSAKLYPIYIIITIIITVGYIMLKNGCRKTKLNT 300
QY 301 ESTPVVEEDMQPYASTYKKNPLDYDTNKVKASQALQSEVPTDITL 348
DB 301 ESTPVVEEDMQPYASTYKKNPLDYDTNKVKASQALQSEVPTDITL 348

RESULT 15
ID AEU92806 standard; protein; 348 AA.
XX AEU92806;
AC AEU92806;
DT 18-JUL-2003 (first entry)
DE Human secreted/transmembrane protein (PRO) #247.
XX Human; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cell; TNF-alpha;
XX tumour necrosis factor-alpha; gene therapy.
OS Homo sapiens.
XX US2003036149-A1.
XX US2003036149-A1.
XX 20-FEB-2003.
XX 02-JUL-2002; 2002US-00187746.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
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XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063544P.
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PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0077450P.
PR 10-MAR-1998; 98US-0077632P.
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PR 20-MAR-1998; 98US-0078886P.
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PR 27-MAR-1998; 98US-0079664P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
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PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
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PR 15-MAY-1998; 98US-0085580P.
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PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0086023P.
PR 18-MAY-1998; 98US-0086332P.
PR 22-MAY-1998; 98US-0086486P.
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PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087509P.
PR 03-JUN-1998; 98US-0087827P.
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PR 05-JUN-1998; 98US-0088167P.
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 PR 17-JUN-1998; 98US-0089655P.
 PR 18-JUN-1998; 98US-0089808P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090254P.
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 PR 24-JUN-1998; 98US-0090432P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 24-JUN-1998; 98US-0090535P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090690P.
 PR 25-JUN-1998; 98US-0090694P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-00105413.
 PR 26-JUN-1998; 98US-0090863P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 26-JUN-1998; 98US-0091010P.
 PR 01-JUL-1998; 98US-0091359P.
 PR 01-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091625P.
 PR 02-JUL-1998; 98US-0091632P.
 PR 02-JUL-1998; 98US-0091632P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 10-AUG-1998; 98US-0095598P.
 PR 10-AUG-1998; 98US-0096012P.
 PR 17-AUG-1998; 98US-0096575P.
 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096867P.
 PR 17-AUG-1998; 98US-0096891P.
 PR 17-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 26-AUG-1998; 98US-0097954P.
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 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 02-SEP-1998; 98US-0098803P.
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 PR 09-SEP-1998; 98US-0098602P.
 PR 10-SEP-1998; 98US-0099741P.
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 PR 10-SEP-1998; 98US-0099763P.
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 PR 16-SEP-1998; 98US-0100664P.
 PR 16-SEP-1998; 98US-0101751P.
 PR 16-SEP-1998; 98US-0101751P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100819P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.

PR 23-SEP-1998; 98US-0101471P.
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 PR 24-SEP-1998; 98US-0101742P.
 PR 25-SEP-1998; 98US-0101786P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102655P.
 PR 06-OCT-1998; 98US-0102588P.
 PR 06-OCT-1998; 98US-0103499P.
 PR 07-OCT-1998; 98US-00168978.

Query Match 99.8%; Score 1843; DB 6; Length 348;
 Best Local Similarity 99.7%; Pred. No. 4.5e-169;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCFRTANIGLILITITFLVAEAGAAPNNSIMLQTSKEMHAAASSICMDEKOTON 60
 DB 1 MLCFRTANIGLILITITFLVAEAGAAPNNSIMLQTSKEMHAAASSICMDEKOTON 60
 QY 61 YSKVLAEVNTSWPVCATNAVLCCPPIALRNLIITFEIILNGOPSCRAYRKEITKE 120
 DB 61 YSKVLAEVNTSWPVCATNAVLCCPPIALRNLIITFEIILNGOPSCRAYRKEITKE 120
 QY 121 TNCIDERITWSPDPNDSIDQIRPAITHDGYRCIMVTPDGNFHHGYHLOVATPEVLT 180
 DB 121 TNCIDERITWSPDPNDSIDQIRPAITHDGYRCIMVTPDGNFHHGYHLOVATPEVLT 180
 QY 181 FQNRRTAVCAKAGPAAQISWIPGDCATKQEYNSNGITVTKSCHEVHVNSTVTC 240
 DB 181 FQNRRTAVCAKAGPAAQISWIPGDCATKQEYNSNGITVTKSCHEVHVNSTVTC 240
 QY 241 VSHLTGKSLYIELLPVPGAKKSAKLYIPYIIITITITVGIWILTKNGCKRYLNT 300
 DB 241 VSHLTGKSLYIELLPVPGAKKSAKLYIPYIIITITITVGIWILTKNGCKRYLNT 300
 QY 301 ESTPVEEDEMOPYASTENFLYDTWNVKASQALOSEVDLHTL 348
 DB 301 ESTPVEEDEMOPYASTENFLYDTWNVKASQALOSEVDLHTL 348

Search completed: May 7, 2004, 11:40:44
 Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 11:39:39 ; Search time 22 Seconds
(without alignments)
816.629 Million cell updates/sec

Title: US-10-009-445A-20

Perfect score: 1846
Sequence: 1 MLCWRTANGLILLITFL.....NKVKASQALQSEVDTLHTL 348Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1822	98.7	348	4	US-09-489-847-211
2	1779	96.4	348	4	US-09-489-847-368
3	1779	96.4	349	4	US-09-489-847-242
4	131	7.1	1091	3	US-08-986-485-5
5	125.5	6.8	479	4	US-09-723-368-2
6	125	6.8	731	1	US-08-070-165F-10
7	125	6.8	731	2	US-08-885-418-10
8	120	6.5	1101	3	US-08-986-485-2
9	117	6.3	458	4	US-09-435-956A-1
10	115	6.2	1253	4	US-08-506-296B-14
11	114.5	6.2	398	4	US-09-778-510-4
12	111	6.0	729	1	US-08-070-165F-6
13	111	6.0	729	2	US-08-885-418-6
14	110.5	6.0	432	4	US-09-778-510-2
15	109.5	5.9	442	4	US-09-778-510-20
16	109.5	5.9	442	4	US-09-930-803-1
17	108.5	5.9	440	4	US-09-866-028-61
18	108.5	5.9	517	4	US-09-723-368-4
19	107.5	5.8	315	4	US-09-910-174B-28
20	107.5	5.8	315	4	US-09-620-461-28
21	107.5	5.8	1059	4	US-09-907-794A-290
22	107.5	5.8	1059	4	US-09-905-125A-290
23	107.5	5.8	1059	4	US-09-902-775A-290
24	107.5	5.8	1119	4	US-09-907-794A-294
25	107.5	5.8	1119	4	US-09-905-125A-294
26	107.5	5.8	1119	4	US-09-902-775A-294
27	105.5	5.7	526	1	US-08-471-570-4

28	105.5	5.7	652	1	US-08-471-570-10	Sequence 10, Appl
29	105	5.7	423	4	US-09-778-510-22	Sequence 22, Appl
30	104.5	5.7	274	4	US-09-570-367C-19	Sequence 19, Appl
31	104.5	5.7	274	4	US-09-915-524-19	Sequence 19, Appl
32	104.5	5.7	763	1	US-08-471-570-6	Sequence 6, Appl
33	104.5	5.7	763	1	US-08-471-570-8	Sequence 8, Appl
34	103.5	5.6	278	4	US-09-570-367C-2	Sequence 2, Appl
35	103.5	5.6	278	4	US-09-915-524-2	Sequence 2, Appl
36	102.5	5.6	434	3	US-09-540-245A-19	Sequence 19, Appl
37	102	5.5	316	4	US-09-910-174B-24	Sequence 24, Appl
38	102	5.5	316	4	US-09-620-461-24	Sequence 24, Appl
39	101.5	5.5	526	4	US-09-910-174B-9	Sequence 9, Appl
40	101.5	5.5	526	4	US-09-620-461-9	Sequence 9, Appl
41	101.5	5.5	1461	4	US-09-976-594-531	Sequence 531, Appl
42	100.5	5.4	398	4	US-09-778-510-6	Sequence 6, Appl
43	100.5	5.4	398	4	US-09-907-794A-84	Sequence 84, Appl
44	100.5	5.4	398	4	US-09-905-125A-84	Sequence 84, Appl
45	100.5	5.4	398	4	US-09-902-775A-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1
US-09-489-847-211
Sequence 211, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031p1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 211
LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
US-09-489-847-211

Query Match 98.7%; Score 1822; DB 4; Length 348;
Best Local Similarity 98.6%; Pred. No. 5,8e-180;
Matches 343; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY	1	MLCPWRTANGLILLITFLVVAEAGAOPNNLSIMLQTSKFNALSSSLCMEKQITON	60
DB	1	MLCPWRTANGLILLITFLVVAEAGAOPNNLSIMLQTSKFNALSSSLCMEKQITON	60
QY	61	YSKVLAEVNTSWPKQATNAVLCCPPIALRNLIITWEIILNRQPSCTAYAKKEINETYE	120
DB	61	YSKVLAEVNTSWPKQATNAVLCCPPIALRNLIITWEIILNRQPSCTAYAKKEINETYE	120
QY	121	TNCTDERITWVSPDQNSDQIRPVAITDGGYRCIMTPDGGFHHGYHLQVLTPEVTL	180
DB	121	TNCTDERITWVSPDQNSDQIRPVAITDGGYRCIMTPDGGFHHGYHLQVLTPEVTL	180
QY	181	FOHNRRAVCAKAVAGRAQISWIPGDCATKQEYNSGTVVKSICMEVHNVSTVTC	240
DB	181	FOHNRRAVCAKAVAGRAQISWIPGDCATKQEYNSGTVVKSICMEVHNVSTVTC	240

Fri May 7 11:49:14 2004

us-10-009-445a-20.fai

Page 2

QY 241 VSHLTGKSLYIELLPVPAKKSAGLYPIIITITITVGFIMLLKNGCRKYNKT 300
DB 241 VSHLTGKSLYIELLPVPAKKSAGLYPIIITITITVGFIMLLKNGCRKYNKT 300
QY 301 ESTPVEEDEMOPYASTEKNNPLDYDTNKKVKSQALQSEVDTDLHTL 348
DB 301 ESTPVEEDEMOPYASTEKNNPLDYDTNKKVKSQALQSEVDTDLHTL 348

RESULT 2
US-09-489-847-368

/ Sequence 368, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ EARLIER FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 368
/ LENGTH: 348
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (283)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (293)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (325)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (326)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-368

Query Match 96.4%; Score 1779; DB 4; Length 348;
Best Local Similarity 96.6%; Pred. No. 1.6e-175;
Matches 336; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLCPEWRTANGLILLITITFLVAEAGAAQPNNSIMLTQSKENHALASSSLCMDEKQTON 60
DB 1 MLCPEWRTANGLILLITITFLVAEAGAAQPNNSIMLTQSKENHALASSSLCMDEKQTON 60
QY 61 YSKYLAENVTSWPKMATNAVLCCPITALRLIIITWEIILRGQPSCTKAYKKEINETKE 120
DB 61 YSKYLAENVTSWPKMATNAVLCCPITALRLIIITWEIILRGQPSCTKAYKKEINETKE 120
QY 121 TNCDEEITWSPRDQSDQIRPVATTHDGYRCIMVTPDGFHGHYLOVLTPEVTL 180
DB 121 TNCDEEITWSPRDQSDQIRPVATTHDGYRCIMVTPDGFHGHYLOVLTPEVTL 180
QY 181 FQNNRTAVCAVAGKPAQISWIPGDCATKQEYNSNGTVYKSTCHWEVHNVSTVCH 240
DB 181 FQNNRTAVCAVAGKPAQISWIPGDCATKQEYNSNGTVYKSTCHWEVHNVSTVCH 240

DB 181 FQNNRTAVCAVAGKPAQISWIPGDCATKQEYNSNGTVYKSTCHWEVHNVSTVCH 240
QY 241 VSHLTGKSLYIELLPVPAKKSAGLYPIIITITITVGFIMLLKNGCRKYNKT 300
DB 241 VSHLTGKSLYIELLPVPAKKSAGLYPIIITITITVGFIMLLKNGCRKYNKT 300
QY 301 ESTPVEEDEMOPYASTEKNNPLDYDTNKKVKSQALQSEVDTDLHTL 348
DB 301 ESTPVEEDEMOPYASTEKNNPLDYDTNKKVKSQALQSEVDTDLHTL 348

RESULT 3
US-09-489-847-242

/ Sequence 242, Application US/09489847
/ Patent No. 6476195
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al
/ TITLE OF INVENTION: 98 Human Secreted Proteins
/ FILE REFERENCE: P2031P1
/ CURRENT APPLICATION NUMBER: US/09/489,847
/ EARLIER FILING DATE: 2000-01-24
/ EARLIER APPLICATION NUMBER: PCT/US99/17130
/ EARLIER FILING DATE: 1999-07-29
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ EARLIER APPLICATION NUMBER: 60/095,486
/ EARLIER FILING DATE: 1998-08-05
/ EARLIER APPLICATION NUMBER: 60/096,319
/ EARLIER FILING DATE: 1998-08-12
/ EARLIER APPLICATION NUMBER: 60/095,454
/ EARLIER FILING DATE: 1998-08-06
/ EARLIER APPLICATION NUMBER: 60/095,455
/ EARLIER FILING DATE: 1998-08-06
/ NUMBER OF SEQ ID NOS: 376
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 242
/ LENGTH: 349
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (283)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (293)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (325)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (326)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-242

Query Match 96.4%; Score 1779; DB 4; Length 349;
Best Local Similarity 96.6%; Pred. No. 1.6e-175;
Matches 336; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 MLCPEWRTANGLILLITITFLVAEAGAAQPNNSIMLTQSKENHALASSSLCMDEKQTON 60
DB 1 MLCPEWRTANGLILLITITFLVAEAGAAQPNNSIMLTQSKENHALASSSLCMDEKQTON 60
QY 61 YSKYLAENVTSWPKMATNAVLCCPITALRLIIITWEIILRGQPSCTKAYKKEINETKE 120
DB 61 YSKYLAENVTSWPKMATNAVLCCPITALRLIIITWEIILRGQPSCTKAYKKEINETKE 120
QY 121 TNCDEEITWSPRDQSDQIRPVATTHDGYRCIMVTPDGFHGHYLOVLTPEVTL 180
DB 121 TNCDEEITWSPRDQSDQIRPVATTHDGYRCIMVTPDGFHGHYLOVLTPEVTL 180
QY 181 FQNNRTAVCAVAGKPAQISWIPGDCATKQEYNSNGTVYKSTCHWEVHNVSTVCH 240
DB 181 FQNNRTAVCAVAGKPAQISWIPGDCATKQEYNSNGTVYKSTCHWEVHNVSTVCH 240

QY 121 TNCBTRITWVSRPQNSDLOIRPAITHDGYRCIMTDPGNHRCYHLOVLTPEVTL 180
DB 121 TNCBTRITWVSRPQNSDLOIRPAITHDGYRCIMTDPGNHRCYHLOVLTPEVTL 180
QY 181 FQNRRTAVCAKPAQIAISWIPEDCATKOEYWSNGTIVKSTCHMEVHNVSTVCH 240
DB 181 FQNRRTAVCAKPAQIAISWIPEDCATKOEYWSNGTIVKSTCHMEVHNVSTVCH 240
QY 241 VSHLTGKSLYIELLPVPGAKSAKLYPIYIIITITIVGFTWLKNGCRRYKNT 300
DB 241 VSHLTGKSLYIELLPVPGAKSAKLYPIYIIITITIVGFTWLKNGCRRYKNT 300
QY 301 ESTPVEDEMOQPYASYTEKNPLDYDTNKKVSAQALQSEVDTDLHTL 348
DB 301 ESTPVEDEMOQPYASYTEKNPLDYDTNKKVSAQALQSEVDTDLHTL 348

RESULT 4
US-08-986-485-5
Sequence 5, Application US/08986485
Patent No. 6046030
GENERAL INFORMATION:
APPLICANT: KU, SHUITAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUBH, ALEKSEED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-986-485-5

Query Match 7.1%; Score 131; DB 3; Length 1091;
Best Local Similarity 23.4%; Pred. No. 0.00031;
Matches 64; Conservative 37; Mismatches 119; Indels 54; Gaps 14;

QY 87 IALRMILITWEIIRGQPSCTKAYKETNETKNTCD-----ERITWVSRPQNSDLO 141
DB 610 IAIKRTGTALECATGHNPNQIAWQKDG-----IDFAAERRNHV-MPDDV-FF 660
QY 142 IRPAVITHDGYRCIMTDPGNHRCYHLOVLTPEVTL-----EVTLPQNRRT 187

DB 661 ITDYKIDMGVISCIAQNSAGSVSANATLTLETSLANPLDEDRVYTGETAFO----- 715
QY 188 AVCAKPAQIAISWIPEDCATKOEYWSNGTIVKSTCHMEVHNVSTVCH 243
DB 716 --CKA-TGSPTFRITWLKGRPLSLTERHFTFGNQLVQVNM--IDAGRYTCEN 769
QY 244 LQNKSLY--IELLPVPGAKSAKLYPIYIIITITIVGFTWLKNGCRRYKNT 297
DB 770 PLTERAHSQSLTLPFGCRKDTGVTGIFTLAVCSVLTSLVWCTIYQTRKSEFYS 829
QY 298 NKTESTPVEDEMOQPYASYTEKNPLDYDTNKKV 331
DB 830 TNDDET-IVPDP---VPSYLSQGTLSDRQETV 858

RESULT 5
US-09-723-368-2
Sequence 2, Application US/09723368
Patent No. 6641818
GENERAL INFORMATION:
APPLICANT: NORTHWESTERN UNIVERSITY
APPLICANT: SPEAR, Patricia G.
APPLICANT: WARNER, Moryn S.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: MARTINEZ, Wanda M.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: COHEN, Gary H.
APPLICANT: EISENBERG, Roselyn J.
APPLICANT: WHITEBECK, Charles J.
APPLICANT: KREUMENACKER, Claude
APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 200290, 0050/201
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. 60/087,862
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ. ID NO 2
LENGTH: 479
TYPE: PRT
ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 6.8%; Score 125.5; DB 4; Length 479;
Best Local Similarity 24.7%; Pred. No. 0.00031;
Matches 53; Conservative 32; Mismatches 87; Indels 43; Gaps 9;

QY 63 KVLAEVNTSWPMKATNANVLC--PPIALRMILITWEIIRGQPSCTKAYR----- 112
DB 37 QVLPBVRG---QLGTVLPLPCHLPVPGLVLSLVTWC-----RDADANQVAAFP 87
QY 113 KETNETKNTCDERITWVSRPD-----QNSDLOIRPAITHDGYRCIMT-PD 161
DB 88 KMPSPSPKPSGERSLFSVSAKOSTGDTAEIQLDITLHLGLTYVEDEGNATCEPFTFK 147
QY 162 GNFRGYHLOVLTPEVTL-----EVTLPQNRRTAVCAKPAQIAISWIPEDCATKOE 214
DB 148 GSVRGMTWLRVIAKPNQAEAGKVTFSOPTVVALCISKEGRPARISWLSISLDEAKET 207
QY 215 YMSN---GTVYKSTCHMEVHNVSTVCHVSH 243
DB 208 QVSGTLGTVVSRPFLVPSGRADGVTGCKVER 242

RESULT 6
US-08-070-165F-10
Sequence 10, Application US/08070165F
Patent No. 5750365
GENERAL INFORMATION:

APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 52052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-070-165F-10

Query Match
Best Local Similarity 22.0%; Score 125; DB 1; Length 731;
Matches 89; Conservative 54; Mismatches 151; Indels 110; Gaps 20;

10 LGLLITLIFLVAEAGAPNNLSMLQTSKENHALASSLCMDKQITQ-----NYSK 63
8 MGLVAVATLTL-----SLAPSYNIADTLLEPEDANSSGDDDDNDGSEDFTDNNHMR 62
64 VLAENVTS-----WPKYATNAVLCCPPIALRNLIITWEILLRGQSPCTKAYKETNE 117
63 APYWTNTEKLEKLAHAPANTYKFCP-----AGNPTPSKRWLNKXKE 107
118 TKEINTDERITWSPDQNSDQIRPVAILTHDGYRCIMTPDGNFHRGYLQVLY-TP 176
108 FKQ---EHRIGCFKRSQHFSLIMESVPSDEGNTCIMENYGSINHTYHLDVERSP 163
177 EYTLFQ---NRNTA-----VCKAVAKPAAQISWI-----PEGD---CAT 211
164 HRPILQAGLPANTTTKVGDAFEVCK-VYSDAQPHQWIRHPELNGSKIGPDGHPYLKVL 222
212 KOEYWSNGITVYKSTGHEVHNVSTV-----TCHVSHLTG--NKSLEYIELLPVPAKAKSA 264
223 KSGINSNAEVLTL-----LHNVTEADRGQYCKVSNYIGEANQSAWLTVLPASEKDEER 277
265 KL-----YIPIITLITLIVGFIMLLKVNCRK-----YKLNKTESTPV- 305
278 ELDSSEYETIAIYCVGFLITCMIGTIWCHKKGKSGKSDSPSPAVHKLKSK--SLPLR 335
306 ---VEEDMQPASYTEKRNPLDYTTNKVKASQALQSEVDTL 345
336 RQVTVSADS-----SSSMNSNTPL-----VRITRLSSNNDTHL 369

RESULT 7
US-08-885-418-10
Sequence 10, Application US/08885418
Patent No. 5925528
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 52052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
COUNTRY: USA
ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-885-418-10

Query Match
Best Local Similarity 22.0%; Score 125; DB 2; Length 731;
Matches 89; Conservative 54; Mismatches 151; Indels 110; Gaps 20;

10 LGLLITLIFLVAEAGAPNNLSMLQTSKENHALASSLCMDKQITQ-----NYSK 63
8 MGLVAVATLTL-----SLAPSYNIADTLLEPEDANSSGDDDDNDGSEDFTDNNHMR 62
64 VLAENVTS-----WPKYATNAVLCCPPIALRNLIITWEILLRGQSPCTKAYKETNE 117
63 APYWTNTEKLEKLAHAPANTYKFCP-----AGNPTPSKRWLNKXKE 107
118 TKEINTDERITWSPDQNSDQIRPVAILTHDGYRCIMTPDGNFHRGYLQVLY-TP 176
108 FKQ---EHRIGCFKRSQHFSLIMESVPSDEGNTCIMENYGSINHTYHLDVERSP 163
177 EYTLFQ---NRNTA-----VCKAVAKPAAQISWI-----PEGD---CAT 211
164 HRPILQAGLPANTTTKVGDAFEVCK-VYSDAQPHQWIRHPELNGSKIGPDGHPYLKVL 222
212 KOEYWSNGITVYKSTGHEVHNVSTV-----TCHVSHLTG--NKSLEYIELLPVPAKAKSA 264
223 KSGINSNAEVLTL-----LHNVTEADRGQYCKVSNYIGEANQSAWLTVLPASEKDEER 277
265 KL-----YIPIITLITLIVGFIMLLKVNCRK-----YKLNKTESTPV- 305
278 ELDSSEYETIAIYCVGFLITCMIGTIWCHKKGKSGKSDSPSPAVHKLKSK--SLPLR 335
306 ---VEEDMQPASYTEKRNPLDYTTNKVKASQALQSEVDTL 345
336 RQVTVSADS-----SSSMNSNTPL-----VRITRLSSNNDTHL 369

RESULT 8
US-08-986-485-2
Sequence 2, Application US/08986485
Patent No. 6046030
GENERAL INFORMATION:
APPLICANT: WU, SHOUJIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: TRUENH, ALEMESEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-986-485-2

Query Match 6.5%; Score 120; DB 3; Length 1101;
Best Local Similarity 23.5%; Pred. No. 0.0043;
Matches 63; Conservative 37; Mismatches 126; Indels 42; Gaps 14;

87 IALRLIITWELIRGQPSCTKAYRKETNETKENCND-----ERTWVRPQNSDLQ 141
Db 616 ITRITTTARLECAATGHPNPQIAWQKDG-----TDFPAERKRAV-MPDDV-FF 666
Qy 142 IRPAVITHDGYRCIMVTPDGNFHRGYHVLVTPVETLFGNNRRTAV-----CKAVA 194
Db 667 ITDVXIDAGVYSCAONSAGSISANATLTLETPLVPLDEDRVSVGETVALQCKA-T 725
Qy 195 GKPAQISWIBEGD---CATQKQVKS--NGTVYKSTCHMEVHVSVTTCVSHLTGNKS 249
Db 726 GNPPRITWF-KGDPISLTERHHTTPNQLLVQNVV--AEDAGRYCEMSWTQTER 781
Qy 250 LYIEV-LPVPGAKSALVYPIILITLITVIGFIWLKVNCRK---YKLNKTEST 303
Db 782 AHSQSVYPAAGCRDGTGVTGIFITAVVSSIVLSVWVCIIYGRKKSSEYSTVNTDET 841
Qy 304 PVEEDENQPYASTYKKNPLYDTTNKY 331
Db 842 -VVPD---VPSYLSQGTLSDRQETV 864

RESULT 9
US-09-435-956A-1
Sequence 1, Application US/09435956A
Patent No. 6469155
GENERAL INFORMATION:
APPLICANT: Universita degli Studi di Bologna
APPLICANT: Institut National de la Sante et de la Recherche M
TITLE OF INVENTION: Hicr and Related V Domain for the Manufacture of a
TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
FILE REFERENCE: MODIANO
CURRENT APPLICATION NUMBER: US/09/435,956A
CURRENT FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: Original Source: Hela Cell line
OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
OTHER INFORMATION: Superfamily
OTHER INFORMATION: Binding Macromolecules: HSV-GD
OTHER INFORMATION: Subcellular Localisation: Plasma Membrane
OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 6.3%; Score 117; DB 4; Length 458;
Best Local Similarity 20.6%; Pred. No. 0.0022;
Matches 54; Conservative 41; Mismatches 113; Indels 54; Gaps 9;

Qy 94 IITWELIRGQPSCTKAYRKETNETKENCNDERTWVRPQNSDLQIRPAVITHDGY 153
Db 182 VSWMETRLKGE-----AEYQEIINPMT---VTVISR-----YRLVPSREARQSL 224
Qy 154 RCIMWTPDGNFHRGYHVLVTPVETL-----FQNNRTAVCAVAKGKPAQISWIP 205
Db 225 ACTIVYHMDRFKESLTIANVQPEVETIEGPDGNWYIQMDVLTCAADANPATEYHWT 284
Qy 206 EGDCAKQKQVWNGTVYKSTCHMEVHVSVTTCVSHLTGNKSLYIEL-----LPVQ 259
Db 285 LNSLPKGVGAQNRITLFFKGPINYSL--AGTYICEATNPIDGRSGQVEVNTKEKPPQK 342
Qy 260 AKSAKLYPIYIITLITLITVIGFIWLKVNCRKYNKTESTPVEEDENQPYASTY 319
Db 343 LGSARLIGTAVAFILVAVLTVPFL-----YKROQKSP-----PETDGAG 384
Qy 320 KNNPLYDTTNKYKASQALQSEV 341
Db 385 TDQPL---SQKPEPSPSRQSSL 403

RESULT 10
US-08-506-296B-14
Sequence 14, Application US/08506296B
Patent No. 6313265
GENERAL INFORMATION:
APPLICANT: Phillips, Greg
APPLICANT: Cunningham, Bruce A.
APPLICANT: Crossin, Kathryn L.
TITLE OF INVENTION: NEURITE OUTGROWTH-PROMOTING POLYPEPTIDES
TITLE OF INVENTION: CONTAINING FIBROBLAST TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: U.S.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,296B
FILING DATE: 24-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 488.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937

QY 308 EDEMOPVASYTEKNNPLDYTTNKVAKASOALQSEVDTL 345
 Db 340 ADS-----SSSMNSNPL-----VATITRLSSNNDTHL 367

RESULT 13
 US-08-885-418-6
 ; Sequence 6, Application US/08885418
 ; Patent No. 5925528
 ; GENERAL INFORMATION:
 ; APPLICANT: CHU, Ing-Ming
 ; APPLICANT: Poulin, Matthew L
 ; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Ing-Ming Chu
 ; STREET: 82052 Davis Medical Research Center, 480 West
 ; STREET: 9th Avenue
 ; CITY: Columbus
 ; STATE: Ohio
 ; COUNTRY: USA
 ; ZIP: 43210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/885,418
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (614)-293-8093
 ; TELEFAX: (614)-293-5631
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 729 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-885-418-6

Query Match 6.0%; Score 111; DB 2; Length 729;
 Best Local Similarity 22.1%; Pred. No. 0.019;
 Matches 88; Conservative 52; Mismatches 156; Indels 100; Gaps 19;

QY 10 LGLILITFLVAEAGAPNNLSIMLQTSKENHALASSSLCMEKQITQ-----NYSK 63
 Db 8 MGLVWVATATL-----SLARPSYNAEDTLEPEDANSSGDDEDNDGSEDFTNNDNHR 62
 QY 64 VLAENVTS-----WPVKATNAVLCPPIALRNLIITWELLIRGQPSCTKARKETNE 117
 Db 63 APYNTNTEKLEKLAHVPAANTVKRCP-----AGNPTEBMRWLNKQKE 107
 QY 118 TKEINTCDERTIWSRPQNSDLQIRPAITHDGYRCIMWTPDGNFRGTHLQVIV-TP 176
 Db 108 FKQ-----EHRIGGFVRSQHFSLIMESVPSDEGNYTCIMENYEGSINHETHLDIVERSP 163
 QY 177 EVTLFQ--NNRRR-----VCKAVAGKPAQISVI-----PEGCAIKQE 214
 Db 164 HRPILQAGLPANTTKVGGDAEFVCK-VYSDAQPHIQIRHFEINSGKIGDGHPIYKVL 222
 QY 215 YMSNGTVTKSTCHWEVAVNS-----TVTCHVSHLTG--NKSLEYELLP-----VPGAKK 262
 Db 223 KAAGVNTDKELVLYVAVNSFPEDAGEYTCLAGNSTGSIYHTALVYLPEBERLDSSE 282
 QY 263 SAKLYIPYIITLITLITVGFILKLVNGCRK-----YKANTBSGPV-----VE 307
 Db 263 YTEINAI-YCVGGFLITTCIGITIMCHMKRGKSDPSSPPAVHKLGR--SHFLRQVTVS 339
 QY 308 EDEMOPVASYTEKNNPLDYTTNKVAKASOALQSEVDTL 345
 Db 340 ADS-----SSSMNSNPL-----VATITRLSSNNDTHL 367

RESULT 14
 US-09-778-510-2
 ; Sequence 2, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778,510
 ; CURRENT FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-778-510-2

Query Match 6.0%; Score 110.5; DB 4; Length 432;
 Best Local Similarity 22.0%; Pred. No. 0.0095;
 Matches 65; Conservative 41; Mismatches 110; Indels 79; Gaps 11;

QY 12 LILILITFLVAEAGAPNNLSIMLQTSKENHALASSSLCMEKQITQNYKVLAVNTS 71
 Db 8 LILILITFLVACCPAPGCA-----NLSQGYWQED-----LEGLTL 42
 QY 72 WPKVATNAVLCPPIALRNLIITW---EILRGPSCTKARKKE-----TNETKE 120
 Db 43 APIDEAISSTWSSPDLMSQSPWTSDETVAGGVTLKQVQDHEDSLQMSNPAQ 102
 QY 121 T-----NCTBERTIWSRPQNSDLQIRPAITHDGYRCIMWTPDGNFRGTHLQVIV-TP 159
 Db 103 TLYFGKRLRDRIQVLTSTHELSISISVNLADSGEYTSIFTMPTAKSLVTVLG 162
 QY 160 -PDGNFRGYHQLVITPEVTLFONKNRTPAVKAVAGKPAQISWIP-----EGDCATYQ 213
 Db 163 IPQKPIITGY-----KSLREKDTATLNCQSSGSKPAARLTKRKQDELHGEPTRIQ 214
 QY 214 EYMSNGTVTKSTCHWEV---HNVSTVYCHVSH--LTG--NKSLEYELLPVG 260
 Db 215 EDPNGKFTVSSVTFQVTRRDDGASIVGSVNHESLKGADRSTSORIEVLVTPPTA 269

RESULT 15
 US-09-778-510-20
 ; Sequence 20, Application US/09778510
 ; Patent No. 6512095
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; TITLE OF INVENTION: Molecules Designated B7L1
 ; FILE REFERENCE: 2844-US
 ; CURRENT APPLICATION NUMBER: US/09/778,510
 ; CURRENT FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: PCT/US99/17906
 ; PRIOR FILING DATE: 1999-08-05
 ; PRIOR APPLICATION NUMBER: 60/095,663
 ; PRIOR FILING DATE: 1998-08-07
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-778-510-20

Query Match 5.9%; Score 109.5; DB 4; Length 442;
 Best Local Similarity 25.4%; Pred. No. 0.012;

Fri May 7 11:49:14 2004

us-10-009-445a-20.ra1

Page 8

Matches 59; Conservative 32; Mismatches 82; Indels 59; Gaps 14;

```

OY 7 ANAVLCCP-IALPNLIITWEIL---RQPSCTAYAKETNETKENC---TDER 127
Db 13 AAAAAAAAAAAGLKRLLILFSAALIPGQONTFTKDVYIIEEVAATTSIQVNSKSDS 72
OY 128 ITWASRPDQ-----NSDQI--RPVATHDGYKCIWTV--PD 161
Db 73 VIQILNPNRQITVFEDPFRPLKDSRFQULNFSSSELKVSITNVNISIDEBRVFCQLYTDPQ 132
OY 162 GNFRHGRHLOVLYTPEVYTLFQNRNRAV-----CAVAGKPAQISVTPBEDCKTX- 212
Db 133 ESYTTL--ITVLPFPNNIMIDIOKDVAEGEIEVNCCTAMASKPATYTRRW-KANTELG 188
OY 213 ---QEYNSNGTJVTKSTCHMEVHANS---TVCHVSH--LTGN--KS,LYIEL 254
Db 189 KSEVEHESD-MYTVTSQMLKAKHKEDDGVFVLCQVEHRAVNSGNLOTCQYILEV 239

```

Search completed: May 7, 2004, 11:43:19
Job time : 24 secs

QY 1 MLCPRRTANLGLILLITITFLVAEAGAAQPNNSLMLQTSKENHALLASSSLCMDEKQITON 60
Db 1 MLCPRRTANLGLILLITITFLVAEAGAAQPNNSLMLQTSKENHALLASSSLCMDEKQITON 60
QY 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
Db 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCDBERTITWSPRPNQSDLOIRPVALTHDGYRCIMVTPDGNFPHGHLQVLTPEVLT 180
Db 121 TNCDBERTITWSPRPNQSDLOIRPVALTHDGYRCIMVTPDGNFPHGHLQVLTPEVLT 180
QY 181 FQNRRTAVCKAVAGKPAQAQISWIPEDCATKQEYWSNGTVTKSTCHWEVHNVSTVTC 240
Db 181 FQNRRTAVCKAVAGKPAQAQISWIPEDCATKQEYWSNGTVTKSTCHWEVHNVSTVTC 240
QY 241 VSHLTGNKSLYIELLPVPGAKKSAGLYPIYIITITITVGFIMLKXNGCKRYKLNKT 300
Db 241 VSHLTGNKSLYIELLPVPGAKKSAGLYPIYIITITITVGFIMLKXNGCKRYKLNKT 300
QY 301 ESTPVEBDEMOPYASYTEKNPXYDTTNKXVASQALQSEVDTDLHTL 348
Db 301 ESTPVEBDEMOPYASYTEKNPXYDTTNKXVASQALQSEVDTDLHTL 348
RESULT 4
US-10-201-858-494
Sequence 494, Application US/10201858
Publication No. US20040038337A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C464
CURRENT FILING DATE: US/10/201, 858
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 494
LENGTH: 348
TYPE: PRT
ORGANISM: Homo Sapien
US-10-201-858-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Pred. No. 1,6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLCPRRTANLGLILLITITFLVAEAGAAQPNNSLMLQTSKENHALLASSSLCMDEKQITON 60
Db 1 MLCPRRTANLGLILLITITFLVAEAGAAQPNNSLMLQTSKENHALLASSSLCMDEKQITON 60
QY 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
Db 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCDBERTITWSPRPNQSDLOIRPVALTHDGYRCIMVTPDGNFPHGHLQVLTPEVLT 180
Db 121 TNCDBERTITWSPRPNQSDLOIRPVALTHDGYRCIMVTPDGNFPHGHLQVLTPEVLT 180
QY 181 FQNRRTAVCKAVAGKPAQAQISWIPEDCATKQEYWSNGTVTKSTCHWEVHNVSTVTC 240
Db 181 FQNRRTAVCKAVAGKPAQAQISWIPEDCATKQEYWSNGTVTKSTCHWEVHNVSTVTC 240
QY 241 VSHLTGNKSLYIELLPVPGAKKSAGLYPIYIITITITVGFIMLKXNGCKRYKLNKT 300
Db 241 VSHLTGNKSLYIELLPVPGAKKSAGLYPIYIITITITVGFIMLKXNGCKRYKLNKT 300
QY 301 ESTPVEBDEMOPYASYTEKNPXYDTTNKXVASQALQSEVDTDLHTL 348
Db 301 ESTPVEBDEMOPYASYTEKNPXYDTTNKXVASQALQSEVDTDLHTL 348
RESULT 5
US-10-205-890-494
Sequence 494, Application US/10205890
Publication No. US20040048334A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C519
CURRENT FILING DATE: US/10/205, 890
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612

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SEQ ID NO 494
LENGTH: 348
TYPE: PRT
ORGANISM: Homo Sapien
US-10-205-890-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Pred. No. 1.6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLLITLIFLVAEAGAAQPNNSLMQTSKFNHALASSLCMDEKQITON 60
DB 1 MLCPRRTANLGLLLITLIFLVAEAGAAQPNNSLMQTSKFNHALASSLCMDEKQITON 60
QY 61 YSKVLAENVTSWPKKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
DB 61 YSKVLAENVTSWPKKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCIDERITWSSRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFHRGYHLQVLTPEVTL 180
DB 121 TNCIDERITWSSRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFHRGYHLQVLTPEVTL 180
QY 181 FQNRRTAVCKAVAGKPAQISWIPBGDCATKQSYNSNGTVYKSTCHWEHNVSTVTC 240
DB 181 FQNRRTAVCKAVAGKPAQISWIPBGDCATKQSYNSNGTVYKSTCHWEHNVSTVTC 240
QY 241 VSHLTGNKSLYIELLPVPGAKSKAKLYPIYIIITLITVGFIMLKVNGCRKYLKNT 300
DB 241 VSHLTGNKSLYIELLPVPGAKSKAKLYPIYIIITLITVGFIMLKVNGCRKYLKNT 300
QY 301 ESTPVEEDEMOPYASYTERKNPLDYDTNKKVKSQALQSEVDTDLHTL 348
DB 301 ESTPVEEDEMOPYASYTERKNPLDYDTNKKVKSQALQSEVDTDLHTL 348

RESULT 6

US-10-208-024-494
Sequence 494, Application US/10208024
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C538
CURRENT APPLICATION NUMBER: US/10/208,024
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 494
LENGTH: 348
TYPE: PRT
ORGANISM: Homo Sapien
US-10-208-024-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Pred. No. 1.6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLLITLIFLVAEAGAAQPNNSLMQTSKFNHALASSLCMDEKQITON 60
DB 1 MLCPRRTANLGLLLITLIFLVAEAGAAQPNNSLMQTSKFNHALASSLCMDEKQITON 60
QY 61 YSKVLAENVTSWPKKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
DB 61 YSKVLAENVTSWPKKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCIDERITWSSRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFHRGYHLQVLTPEVTL 180
DB 121 TNCIDERITWSSRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFHRGYHLQVLTPEVTL 180
QY 181 FQNRRTAVCKAVAGKPAQISWIPBGDCATKQSYNSNGTVYKSTCHWEHNVSTVTC 240
DB 181 FQNRRTAVCKAVAGKPAQISWIPBGDCATKQSYNSNGTVYKSTCHWEHNVSTVTC 240
QY 241 VSHLTGNKSLYIELLPVPGAKSKAKLYPIYIIITLITVGFIMLKVNGCRKYLKNT 300
DB 241 VSHLTGNKSLYIELLPVPGAKSKAKLYPIYIIITLITVGFIMLKVNGCRKYLKNT 300
QY 301 ESTPVEEDEMOPYASYTERKNPLDYDTNKKVKSQALQSEVDTDLHTL 348
DB 301 ESTPVEEDEMOPYASYTERKNPLDYDTNKKVKSQALQSEVDTDLHTL 348

RESULT 7

US-10-201-853-494
Sequence 494, Application US/10201853
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C465
CURRENT APPLICATION NUMBER: US/10/201,853
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541

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PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 494
LENGTH: 348
TYPE: PRI
ORGANISM: Homo Sapien
US-10-201-853-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Freq. No. 1,66-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRNTANLGLILITLITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEKQITON 60
DB 1 MLCPRNTANLGLILITLITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEKQITON 60
QY 61 YSKVLAENVTSMPVMAATNAVLCCEPILARNLIIITWEIIIRGQPSCTKAYRKETNETKE 120
DB 61 YSKVLAENVTSMPVMAATNAVLCCEPILARNLIIITWEIIIRGQPSCTKAYRKETNETKE 120
QY 121 TNCDEBRTIWTWRPQNSDLQIRPVAITHDGYRCIMWTPDGNHFGYHLQVLTPEVTL 180
DB 121 TNCDEBRTIWTWRPQNSDLQIRPVAITHDGYRCIMWTPDGNHFGYHLQVLTPEVTL 180
QY 121 TNCDEBRTIWTWRPQNSDLQIRPVAITHDGYRCIMWTPDGNHFGYHLQVLTPEVTL 180
DB 121 TNCDEBRTIWTWRPQNSDLQIRPVAITHDGYRCIMWTPDGNHFGYHLQVLTPEVTL 180
QY 181 FQNRRTAVCAVAKPAQISWIPEDGCATKQEWNSGTVTVYSTGMEVHNSTVTC 240
DB 181 FQNRRTAVCAVAKPAQISWIPEDGCATKQEWNSGTVTVYSTGMEVHNSTVTC 240
QY 241 VSHLGNLSIVTELLFVVGAKKSAKLYPYIILITIIITGFIWMLKNGCRKXKNT 300
DB 241 VSHLGNLSIVTELLFVVGAKKSAKLYPYIILITIIITGFIWMLKNGCRKXKNT 300
QY 301 ESTPVEDEMOFYASYTEKNPLVDITNKVYASQALQSEVDTDLHTL 348
DB 301 ESTPVEDEMOFYASYTEKNPLVDITNKVYASQALQSEVDTDLHTL 348

RESULT 8
US-10-174-581-494
Sequence 494, Application US/10174581
Publication No. US20030017540A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jien
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C41
CURRENT APPLICATION NUMBER: US/10/174,581
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052566
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/07632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078866
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22

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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087098
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088722
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088740

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088811
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088825
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088863
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089090
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Pred. No. 1,6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRFANIGLILITFLVABEAGAAQPNNSLMQTSKRNALASSICMEKQITON 60
DB 1 MLCPRFANIGLILITFLVABEAGAAQPNNSLMQTSKRNALASSICMEKQITON 60
QY YSKVLAENVTSWPKMATNVLCCPPIALNLIITWEIILRGOPSCTKAYREINETKE 120
DB YSKVLAENVTSWPKMATNVLCCPPIALNLIITWEIILRGOPSCTKAYREINETKE 120
QY 121 TNCDEBITWSSRDQSDIQRPAITHDGYRCIMWPDGPHRGYHQUVTPBVL 180
DB 121 TNCDEBITWSSRDQSDIQRPAITHDGYRCIMWPDGPHRGYHQUVTPBVL 180
QY 181 FQNNRTAVCKAVAGKRAQISMPEDGCAKQKQVNSGTIVYKSTCHWEHNVSTVCH 240
DB 181 FQNNRTAVCKAVAGKRAQISMPEDGCAKQKQVNSGTIVYKSTCHWEHNVSTVCH 240
QY 241 VSHLTGKSLYIELLPVGAKKSAKIYPIIITITITVGSFWLKNNGCKRYLNT 300
DB 241 VSHLTGKSLYIELLPVGAKKSAKIYPIIITITITVGSFWLKNNGCKRYLNT 300
QY 301 ESTPVEDEDEMPYASTETKNPLXDTTNVKAQALQSEVDIDLTL 348
DB 301 ESTPVEDEDEMPYASTETKNPLXDTTNVKAQALQSEVDIDLTL 348

RESULT 9
US-10-176-483-494
Sequence 494; Application US/10176483
Publication No. US20030017541A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C68
CURRENT APPLICATION NUMBER: US/10/176,483
CURRENT FILING DATE: 2002-06-20
Prior application removed - See file wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 494
LENGTH: 348
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-483-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Pred. No. 1.6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEDEKQITON 60
DB 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEDEKQITON 60
QY 61 YSKVLAENVTSMPVKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
DB 61 YSKVLAENVTSMPVKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCEDERTITWSPDPQNSDLQIRPVAITHDGYRCIMVDPGNFHRGYHLQVLTPEVTL 180
DB 121 TNCEDERTITWSPDPQNSDLQIRPVAITHDGYRCIMVDPGNFHRGYHLQVLTPEVTL 180
QY 181 FQNRRTAVCKAVAGKPAQISWIEPGDCAKQEWMSGTIVKSTCHMEVHNVSTVTC 240
DB 181 FQNRRTAVCKAVAGKPAQISWIEPGDCAKQEWMSGTIVKSTCHMEVHNVSTVTC 240
QY 241 VSHLTGKNSLYTELLPVPKAKSACLIPYIITLITIGFIMLLKVGCRKRYKLNKT 300
DB 241 VSHLTGKNSLYTELLPVPKAKSACLIPYIITLITIGFIMLLKVGCRKRYKLNKT 300
QY 301 ESTPVVEDEMPYASYTEKNPLDYDTNKKVASQALQSEVDTDLHTL 348
DB 301 ESTPVVEDEMPYASYTEKNPLDYDTNKKVASQALQSEVDTDLHTL 348

RESULT 10
US-10-176-749-494

Sequence 494, Application US/10176749
Publication No. US20030017542A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C68

CURRENT APPLICATION NUMBER: US/10/176,749

Prior application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 494

LENGTH: 348

TYPE: PRT

ORGANISM: Homo Sapien

US-10-176-749-494

Query Match 99.8%; Score 1843; DB 12; Length 348;

Best Local Similarity 99.7%; Pred. No. 1.6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEDEKQITON 60
DB 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEDEKQITON 60
QY 61 YSKVLAENVTSMPVKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
DB 61 YSKVLAENVTSMPVKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCEDERTITWSPDPQNSDLQIRPVAITHDGYRCIMVDPGNFHRGYHLQVLTPEVTL 180
DB 121 TNCEDERTITWSPDPQNSDLQIRPVAITHDGYRCIMVDPGNFHRGYHLQVLTPEVTL 180
QY 181 FQNRRTAVCKAVAGKPAQISWIEPGDCAKQEWMSGTIVKSTCHMEVHNVSTVTC 240
DB 181 FQNRRTAVCKAVAGKPAQISWIEPGDCAKQEWMSGTIVKSTCHMEVHNVSTVTC 240
QY 241 VSHLTGKNSLYTELLPVPKAKSACLIPYIITLITIGFIMLLKVGCRKRYKLNKT 300
DB 241 VSHLTGKNSLYTELLPVPKAKSACLIPYIITLITIGFIMLLKVGCRKRYKLNKT 300
QY 301 ESTPVVEDEMPYASYTEKNPLDYDTNKKVASQALQSEVDTDLHTL 348
DB 301 ESTPVVEDEMPYASYTEKNPLDYDTNKKVASQALQSEVDTDLHTL 348

RESULT 11
US-10-176-914-494

Sequence 494, Application US/10176914
Publication No. US20030017543A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3430R1C68

CURRENT APPLICATION NUMBER: US/10/176,914

CURRENT FILING DATE: 2002-06-20

Prior application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 494

LENGTH: 348

TYPE: PRT

ORGANISM: Homo Sapien

US-10-176-914-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
Best Local Similarity 99.7%; Pred. No. 1.6e-167;
Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEDEKQITON 60
DB 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALLASSSLCMEDEKQITON 60
QY 61 YSKVLAENVTSMPVKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
DB 61 YSKVLAENVTSMPVKATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
QY 121 TNCEDERTITWSPDPQNSDLQIRPVAITHDGYRCIMVDPGNFHRGYHLQVLTPEVTL 180
DB 121 TNCEDERTITWSPDPQNSDLQIRPVAITHDGYRCIMVDPGNFHRGYHLQVLTPEVTL 180

QY 181 FQNRRTAVCAVAGKPAQISWIEGDCATKQEWNSGTVTKSTCHEVHNVSTVTC 240
 DB 181 FQNRRTAVCAVAGKPAQISWIEGDCATKQEWNSGTVTKSTCHEVHNVSTVTC 240
 QY 241 VSHLTGNSLYIELLPVPGAKKSALYIPYIIITIIITVGFIMLLKVNCGCRKYLKNT 300
 DB 241 VSHLTGNSLYIELLPVPGAKKSALYIPYIIITIIITVGFIMLLKVNCGCRKYLKNT 300
 QY 301 ESTPVEEDEMOPVASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPVASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL 348

RESULT 12
 US-10-176-915-494
 ; Sequence 494, Application US/10176915
 ; Publication No. US20030017544A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C10
 ; CURRENT APPLICATION NUMBER: US/10/176,915
 ; PRIORITY FILING DATE: 2002-06-21
 ; NUMBER OF SEQ ID NOS: 612
 ; Prior Application removed - See File Wrapper or Palm
 ; SEQ ID NO 494
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-915-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
 Best Local Similarity 99.7%; Pred. No. 1,6e-167;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLCWRTANIGLLIIITFIVAEAGAAOPNNSIMLOTSEKNAALASSLCMDKQITON 60
 DB 1 MLCWRTANIGLLIIITFIVAEAGAAOPNNSIMLOTSEKNAALASSLCMDKQITON 60
 QY 61 YSKYLAENVTSWPKAATNVLCCPITALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 DB 61 YSKYLAENVTSWPKAATNVLCCPITALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 QY 121 TNCIDERITWVSRPDQNSDIQIRPAITHDGYRCIVTPDGNHFGYHLQVLTPEVTL 180
 DB 121 TNCIDERITWVSRPDQNSDIQIRPAITHDGYRCIVTPDGNHFGYHLQVLTPEVTL 180
 QY 181 FQNRRTAVCAVAGKPAQISWIEGDCATKQEWNSGTVTKSTCHEVHNVSTVTC 240
 DB 181 FQNRRTAVCAVAGKPAQISWIEGDCATKQEWNSGTVTKSTCHEVHNVSTVTC 240
 QY 241 VSHLTGNSLYIELLPVPGAKKSALYIPYIIITIIITVGFIMLLKVNCGCRKYLKNT 300
 DB 241 VSHLTGNSLYIELLPVPGAKKSALYIPYIIITIIITVGFIMLLKVNCGCRKYLKNT 300
 QY 301 ESTPVEEDEMOPVASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPVASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL 348

RESULT 13
 US-10-176-484-494

; Sequence 494, Application US/10176484
 ; Publication No. US20030059876A3
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C64
 ; CURRENT APPLICATION NUMBER: US/10/176,484
 ; PRIORITY FILING DATE: 2002-06-20
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 484
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-484-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
 Best Local Similarity 99.7%; Pred. No. 1,6e-167;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLCWRTANIGLLIIITFIVAEAGAAOPNNSIMLOTSEKNAALASSLCMDKQITON 60
 DB 1 MLCWRTANIGLLIIITFIVAEAGAAOPNNSIMLOTSEKNAALASSLCMDKQITON 60
 QY 61 YSKYLAENVTSWPKAATNVLCCPITALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 DB 61 YSKYLAENVTSWPKAATNVLCCPITALRNLIITWEIILRGQPSCTKAYRKETNETKE 120
 QY 121 TNCIDERITWVSRPDQNSDIQIRPAITHDGYRCIVTPDGNHFGYHLQVLTPEVTL 180
 DB 121 TNCIDERITWVSRPDQNSDIQIRPAITHDGYRCIVTPDGNHFGYHLQVLTPEVTL 180
 QY 181 FQNRRTAVCAVAGKPAQISWIEGDCATKQEWNSGTVTKSTCHEVHNVSTVTC 240
 DB 181 FQNRRTAVCAVAGKPAQISWIEGDCATKQEWNSGTVTKSTCHEVHNVSTVTC 240
 QY 241 VSHLTGNSLYIELLPVPGAKKSALYIPYIIITIIITVGFIMLLKVNCGCRKYLKNT 300
 DB 241 VSHLTGNSLYIELLPVPGAKKSALYIPYIIITIIITVGFIMLLKVNCGCRKYLKNT 300
 QY 301 ESTPVEEDEMOPVASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPVASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL 348

RESULT 14
 US-10-180-550-494
 ; Sequence 494, Application US/10180550
 ; Publication No. US2003006440A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1C149
 CURRENT APPLICATION NUMBER: US/10/180,550
 CURRENT FILING DATE: 2002-06-25
 Prior application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 494
 LENGTH: 348
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-180-550-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
 Best Local Similarity 99.7%; Pred. No. 1.6e-167;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSMLQTSKENHALASSSLCMEDEKQITON 60
 DB 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSMLQTSKENHALASSSLCMEDEKQITON 60
 QY 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGOPSCTKAYRKETNETKE 120
 DB 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGOPSCTKAYRKETNETKE 120
 QY 121 TNCCTDERITWVSRRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFRGHYLOVLVPEVTL 180
 DB 121 TNCCTDERITWVSRRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFRGHYLOVLVPEVTL 180
 QY 181 FQNRRTAVCKAVAGKPAQISMIPEGDCATKOEYWSNGTVTKSCHEVNAVSTVTC 240
 DB 181 FQNRRTAVCKAVAGKPAQISMIPEGDCATKOEYWSNGTVTKSCHEVNAVSTVTC 240
 QY 241 VSHLTGNKSLYELLPVPAKKSATLYPIYIILITVIGFIWLKNGCRKXKNT 300
 DB 241 VSHLTGNKSLYELLPVPAKKSATLYPIYIILITVIGFIWLKNGCRKXKNT 300
 QY 301 ESTPVEEDEMOPYASYTEKNNPLYDTTNKVASQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPYASYTEKNNPLYDTTNKVASQALQSEVDTDLHTL 348

RESULT 15
 US-10-183-014-494
 Sequence 494, Application US/10183014
 Publication No. US2003006441A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C170
 CURRENT APPLICATION NUMBER: US/10/183,014
 CURRENT FILING DATE: 2002-06-26
 Prior application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 494
 LENGTH: 348
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-183-014-494

Query Match 99.8%; Score 1843; DB 12; Length 348;
 Best Local Similarity 99.7%; Pred. No. 1.6e-167;
 Matches 347; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSMLQTSKENHALASSSLCMEDEKQITON 60
 DB 1 MLCPRRTANLGLLILITFLVAEAGAAQPNNSMLQTSKENHALASSSLCMEDEKQITON 60
 QY 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGOPSCTKAYRKETNETKE 120
 DB 61 YSKVLAENVTSMPVMAATNAVLCCPPIALRNLIITWEIILRGOPSCTKAYRKETNETKE 120
 QY 121 TNCCTDERITWVSRRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFRGHYLOVLVPEVTL 180
 DB 121 TNCCTDERITWVSRRPDQNSDLQIRPVALTHDGYRCIMVTPDGNFRGHYLOVLVPEVTL 180
 QY 181 FQNRRTAVCKAVAGKPAQISMIPEGDCATKOEYWSNGTVTKSCHEVNAVSTVTC 240
 DB 181 FQNRRTAVCKAVAGKPAQISMIPEGDCATKOEYWSNGTVTKSCHEVNAVSTVTC 240
 QY 241 VSHLTGNKSLYELLPVPAKKSATLYPIYIILITVIGFIWLKNGCRKXKNT 300
 DB 241 VSHLTGNKSLYELLPVPAKKSATLYPIYIILITVIGFIWLKNGCRKXKNT 300
 QY 301 ESTPVEEDEMOPYASYTEKNNPLYDTTNKVASQALQSEVDTDLHTL 348
 DB 301 ESTPVEEDEMOPYASYTEKNNPLYDTTNKVASQALQSEVDTDLHTL 348

Search completed: May 7, 2004, 11:48:07
 Job time : 49 secs

Db 770 PIGTERAHSQSLIPRPGKRGDTGTFITIAVCSIVLISLVWCIITVQRKXSEESV 829

QY 298 NKTESTPVEDEMDQPYASYTEKNPLDYTNKV 331
Db 830 TWTDETF-IVPD-----VPSYLSQGLSPDRQETV 858

RESULT 2

HLMSP3

Poliiovirus receptor homolog precursor - mouse

C/Species: Mus musculus domesticus (western European house mouse)

C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

C/Accession: A38211

R/Morrison, M.E.; Racanelli, V.R.

J/Virology 66:2807-2813, 1992

A/Title: Molecular cloning and expression of a murine homolog of the human poliovirus re

A/Reference number: A38211; MUID:92219365; PMID:1560525

A/Accession: A38211

A/Molecule type: DNA

A/Residues: 1-467 <MOR>

A/Cross-references: GB:M80206; NID:G199785; PIDN:AAA9734.1; PID:G199786

C/Superfamily: poliovirus receptor; immunoglobulin homology

C/Keywords: duplication; glycoprotein; transmembrane protein

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-467/Product: poliovirus receptor homolog #status predicted <MAT>

F/46-354/Domain: extracellular #status predicted <IMM1>

F/47-133/Domain: immunoglobulin homology <IMM2>

F/167-322/Domain: immunoglobulin homology <IMM3>

F/355-374/Domain: transmembrane #status predicted <TMN>

F/375-467/Domain: intracellular #status predicted <INT>

F/54-131,174-229,274-320/Disulfide bonds: #status predicted

F/128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 125.5; DB 1; Length 467;
Best Local Similarity 26.2%; Pred. No. 0.013;
Matches 59; Conservative 37; Mismatches 82; Indels 47; Gaps 14;

QY 63 KTLAEVNTSMVQKATNAVLCC--PPIALRNLIITWE-----ILRGQPSCTKAYRKE 114
Db 37 RVLPEVRG---RLGGTVELPCHLPPPTTER-VSQVTWQGLDGTVAAPHFSPGVDF-- 88

QY 115 TNETKTNCTDERITWY-SRPDQNSDLO-----IRPAITHDGYRCIMWT-PDGNFHRG 167
Db 89 ----PNSQFSKDLSTFRARPEFTNADLRDTLAFRLGRVDEGNYTCERATFPNGTRGV 144

QY 168 YHLOVLVTP-----EVLTFQNRNRTAVCKAVAGKPAQISWPE--GDCAIQOEYW-S 217
Db 145 TWLRVIAQPEHNAEAQEVITIGPQSAVAVACVSTGGRPARITWISLGGKADQDEPGIQ 204

QY 218 NGVTYKSTCHMEVHNVS-----TYTCHVSHLGNKSLYIELLPV 257
Db 205 AGVTITIS--RYSLVPGRADGVKVTGRVHESFEETP---LPLV 244

RESULT 3

IS3960

PRR2 alpha - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C/Accession: I53960

R/Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.

Gene 159, 267-272, 1995

A/Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th

A/Reference number: I53960; MUID:95347610; PMID:7622062

A/Accession: I53960

A/Status: preliminary; translated from GB/EMBL/DBD3

A/Molecule type: mRNA

A/Residues: 1-478 <RES>

A/Cross-references: GB:579171; NID:G1042202; PID:G1042203

C/Genetics:

A/Gene: PRR2alpha

C/Superfamily: poliovirus receptor; immunoglobulin homology

F/276-331/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 125.5; DB 2; Length 478;
Best Local Similarity 24.7%; Pred. No. 0.013;
Matches 53; Conservative 32; Mismatches 87; Indels 43; Gaps 9;

QY 63 KTLAEVNTSMVQKATNAVLCC--PPIALRNLIITWEIIIRGQPSCTKAYR----- 112
Db 37 QVLPEVRG---RLGGTVELPCHLPPVRLYISLVWQ-----RBDAPAHQVAAFRP 87

QY 113 KENETKTNCTDERITWYSPD-----QNSDLOIRPAITHDGYRCIMWT-PD 161
Db 88 KMGSPSPKRGSEERLSFVSAKQSTQDTEALQDRLHLGLTVDEGNYTCERATFPK 147

QY 162 GNPHRGYHLOVLVTP-----EVLTFQNRNRTAVCKAVAGKPAQISWIPEDCATKOE 214
Db 148 GSVKGMWMLVIAKPKQAQKVTSPQDEPTVALCISKGRPPARITWISLSDWEAKET 207

QY 215 YMSN---GTYTYSKSTCHMEVHNVS---TYTCHVSH 243
Db 208 QVSGTLAGVTYVSRFTLVPSGRADGVYTCVKEH 242

RESULT 4

A53437

Poliiovirus receptor mPVR - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C/Accession: A53437

R/Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.

J/Biol. Chem. 269, 8431-8438, 1994

A/Title: Amino acid residues on human poliovirus receptor involved in interaction with

A/Reference number: A53437; MUID:94179228; PMID:8132559

A/Accession: A53437

A/Molecule type: mRNA

A/Residues: 1-530 <AOK>

A/Cross-references: GB:D26107; NID:G475017; PIDN:BA05103.1; PID:G825507

A/Experimental source: C57/BL6, brain

A/Note: sequence extracted from NCBI database (NCBI:146664, NCBI:146667)

C/Superfamily: poliovirus receptor; immunoglobulin homology

F/47-133/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 125.5; DB 2; Length 530;
Best Local Similarity 26.2%; Pred. No. 0.015;
Matches 59; Conservative 37; Mismatches 82; Indels 47; Gaps 14;

QY 63 KTLAEVNTSMVQKATNAVLCC--PPIALRNLIITWE-----ILRGQPSCTKAYRKE 114
Db 37 RVLPEVRG---RLGGTVELPCHLPPPTTER-VSQVTWQGLDGTVAAPHFSPGVDF-- 88

QY 115 TNETKTNCTDERITWY-SRPDQNSDLO-----IRPAITHDGYRCIMWT-PDGNFHRG 167
Db 89 ----PNSQFSKDLSTFRARPEFTNADLRDTLAFRLGRVDEGNYTCERATFPNGTRGV 144

QY 168 YHLOVLVTP-----EVLTFQNRNRTAVCKAVAGKPAQISWPE--GDCAIQOEYW-S 217
Db 145 TWLRVIAQPEHNAEAQEVITIGPQSAVAVACVSTGGRPARITWISLGGKADQDEPGIQ 204

QY 218 NGVTYKSTCHMEVHNVS-----TYTCHVSHLGNKSLYIELLPV 257
Db 205 AGVTITIS--RYSLVPGRADGVKVTGRVHESFEETP---LPLV 244

RESULT 5

IS6093

PRR2 delta - human

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C/Accession: IS6093

R/Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.

Gene 159, 267-272, 1995

A/Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is cl

A:Reference number: I53960; MUID:95347610; PMID:7622062
A:Accession: I68093
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-538 <RES>
A:Cross-references: GB:S79172; NID:G1042204; PID:G1042205
C:Genetics:
A:Gene: FRK2delta
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 125.5; DB 2; Length 538;
Best Local Similarity 24.7%; Pred. No. 0.015;
Matches 53; Conservative 32; Mismatches 87; Indels 43; Gaps 9;

QY 63 KYLAENVTSWPKXATNAVLCC--PPLALNLIITWEILLRQPSCTKAYR-----112
DB 37 QVLPEVRG---QLGQVELPCHLLPVPGLYISLVTWQ---RPDAPAHQVAFHP 87
QY 113 KETNETKNTCTDRITVSRPD-----QNSDLQIRPAITHDGYRCIMWT-PD 161
DB 88 KMGDSFSPKPGSESLSFVSAKQSTGQDTEALDQATLHGLTVEDEGNTCEPATFPK 147
QY 162 GNPHRGYALQVLTVP-----EYTLFQNRNRTAVCKAVAGKPAQISWIPEDCATKOE 214
DB 148 GSVAGMTLRYIAKPKQAEAKQTFESQDPTTVALCISKGRPPARISWLSLDMKERT 207
QY 215 YWSN---GTTVKSTCMEVHANS---TITCVSH 243
DB 208 QVSGTLAQTIVTSTRFLTVPSRGADQVTVTCKVEH 242

RESULT 6

S41051
fibroblast growth factor receptor-2 - eastern newt
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S41051
R:Poulin, M.L.; Chiu, I.M.
Biochim. Biophys. Acta 1220, 209-211, 1994
A:Title: Nucleotide sequences of two new nt (Notophthalmus viridescens) fibroblast growth
A:Reference number: S41050; MUID:9416117; PMID:8312364
A:Accession: S41051
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-750 <POU>
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
F:101-162/Domain: immunoglobulin homology <IMM>
F:408-693/Domain: protein kinase homology <KIN>

Query Match 6.8%; Score 125; Length 750;
Best Local Similarity 22.0%; Pred. No. 0.025;
Matches 89; Conservative 54; Mismatches 151; Indels 110; Gaps 20;

QY 10 LGLLILITFLVAEFGAOPNNSMLQTSKEMALSSLCMEKQITQ-----NYSK 63
DB 27 MGLVAVAAATL---SLARPSYNAEDTLEPEDANSSGDEDDNDGSEDFITDNNHR 81
QY 64 VLAENVTS-----WPKATNAVLCCPPLALNLIITWEILLRQPSCTKAYRKETNE 117
DB 82 APYNTETLEKELKHAVPAAVTVPKRCP-----AGNPPTSMTWLKXGKE 126
QY 118 TKEINCTDERITWVSRPQNSDLQIRPAITHDGYRCIMWTPOGNHRRHGLQVLT-P 176
DB 127 FKQ---BHRIGGFVRSQHSLINESVVPDSDEGYTCIMENEXGSHNTHLIDLVVERSP 182
QY 177 EYTLFQ---NRNRTA-----VCKAVAGKPAQISWI-----PEGD---CAT 211
DB 193 HRPITQAGLPANTTKVGDFAFVCK-VYSDAGPHICWIRFELNGSKIGDGHPIYKVL 241
QY 212 KOEWSNGTIVYKSTCMEVHANSV---TCHVSHITG---NKSLEYELLVPFGAKKA 264
DB 242 KKSGLNNSNAEYLT---LHNVTADAGQYTCVKSNIYIGANOSAWLTVLPASEKDEER 296

QY 265 KL-----YIPYILITLITIVGFIWLKVGNGCRK-----YKLNKTESGPV- 305
DB 297 ELDSSEYEYEAIVYCGVGLITCMIGTIVWCHMKGRGKSDSPPAVKLSK--SLPLR 354
QY 306 ----VEDEMGYPASTEKNNFLYDTTNKVKASQALQSPVDPL 345
DB 355 RQVTVSADS-----SSGMSNTPF-----VRITRLSSNNDTHL 388

RESULT 7

U3BNC
neural cell adhesion molecule short domain form precursor - bovine
N:Alternate names: NCAM-140
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C:Accession: A32976; A38778; B44290; S05402
R:Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Rak;
FEBS Lett. 254, 69-73, 1989

A:Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A:Reference number: A32976; MUID:89378239; PMID:2776887
A:Accession: A32976
A:Molecule type: mRNA
A:Residues: 1-853 <LIP>
A:Cross-references: GB:X16451; NID:960; PID:CAA34470.1; PID:961

A:Accession: A38778
A:Molecule type: protein
A:Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-552
A:Note: The authors identified this protein as calmodulin-independent adenylate cyclase
J. Rougon, G.; Marshak, D.R.
U. Biol. Chem. 261, 3396-3401, 1986

A:Title: Structural and immunological characterization of the amino-terminal domain of r
A:Reference number: A44290; MUID:86140120; PMID:3512556
A:Accession: B44290

A:Molecule type: protein
A:Residues: 20-36 <ROU>
A:Note: 23-Glu was also found

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mo
C:Superfamily: Various forms of NCAM are produced by alternative splicing.
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-853/Product: neural cell adhesion molecule, short domain form #status experimental
F:20-719/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:228-288/Domain: immunoglobulin homology <IMM3>
F:261-870/Region: NCAM binding #status predicted
F:321-396/Domain: immunoglobulin homology <IMM4>
F:428-490/Domain: immunoglobulin homology <IMM5>
F:557-604/Domain: fibronectin type III repeat homology <FN3A>
F:633-693/Domain: fibronectin type III repeat homology <FN3B>
F:720-737/Domain: transmembrane #status predicted <TM>
F:748-853/Domain: intracellular #status predicted <INT>
F:41-96;139-189;235-286;328-354;435-486/Disulfide bonds: #status predicted
F:222;314;346;432;458;487/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 6.6%; Score 122.5; DB 1; Length 853;
Best Local Similarity 22.2%; Pred. No. 0.047;
Matches 65; Conservative 39; Mismatches 102; Indels 87; Gaps 13;

QY 31 NNSLMLQTSK-----ENHALASSSLCMEKQITQ-----YKLAENVTSMP 73
DB 171 NNYLQIRGKTKDDEGYRCGRILRGEINFKDIOYVAVPPTVOARQSI VAVTALGQS 230
QY 74 VKMATNAVLCCPPLALNLIITWEILLRQPSCTKAYRKETNETCTDERITWVSR 133
DB 231 VTLVCNA-----EGPEPTVSWTKDEQLE--NEEDKYL--- 264
QY 134 PDNSDLQIRPAITHDGYRCIMWTPOGNHRRHGLQVLTVPFVTLFQNRK----- 186

Db 265 SDDSELTIRKVDKNDSEAEVYCIENKAGEQDASIHAKVFAKPIYVENQFAMELEBOV 324
 QY 187 TAVCKAVAGPAAQISWIPREGDATKOE--YWS-----NGTVYVSTCHMEVHNVST 236
 Db 325 TLTCFA-SGDFISITWRSTNISTSEKASWTRPEKQETLDGHVVRSHA-----RVSS 378
 QY 237 VT-----CHVSHLNG--NKSLEYIELLPVPGAKSKAKUYIPIYILT 274
 Db 379 LTKSIQYTDAGEVYCTASVTIGDSQSWLYEVQYAP-----KLGQPVAVYT 425

RESULT 8

UCHUNG
 neural cell adhesion molecule 1 GPI-anchored splice form precursor, muscle-specific - hu
 N:Alternate names: CD56; NCAM-120
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1993 #sequence_rev: 31-Mar-1993 #text_change 28-Jan-2000
 C:Accession: S07784; A26883
 R:Baron, C.H.; Dickson, G.; Gower, H.J.; Rowett, L.H.; Putt, W.; Elsom, V.; Moore, S.E.
 Development 104, 165-173, 1988
 A:Title: Complete sequence and in vitro expression of a tissue-specific phosphatidylinositol
 A:Reference number: S07784; MUID:89305258; PMID:3353057
 A:Accession: S07784
 A:Molecule type: mRNA
 A:Residues: 1761 <BAR>
 A:Cross-references: EMBL:X16841; NID:g35005; PIDN:CAA34739.1; PID:g35006
 R:Jackson, G.; Gower, H.J.; Barton, C.H.; Prentice, H.M.; Elsom, V.L.; Moore, S.E.; Cox,
 Cell 50, 119-1130, 1987
 A:Title: Human muscle neural cell adhesion molecule (N-CAM): identification of a muscle-
 A:Reference number: A90895; MUID:87301755; PMID:2887295
 A:Accession: A26883
 A:Molecule type: mRNA
 A:Residues: 421-761 <DIC>
 A:Cross-references: GB:M17409; NID:g189097; PIDN:AAA59912.1; PID:g386979
 A:Comment: NCM mediates cell-cell adhesion via homophilic binding with another NCM mol
 C:Comment: Various forms of NCM are produced by alternative splicing.
 C:Genetics:
 A:Gene: GDB:NCAM1; NCAM; CD56
 A:Cross-references: GDB:119448; OMIM:116930
 A:Map position: 11q22.2-11q22.3
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
 F:1/19/Domain: signal sequence #status predicted <Sig>
 F:20-761/Product: neural cell adhesion molecule phosphatidylinositol-linked form, muscle
 F:34-98/Domain: immunoglobulin homology <IMM1>
 F:132-191/Domain: immunoglobulin homology <IMM2>
 F:152-156/Region: heparin binding #status predicted
 F:161-165/Region: heparin binding #status predicted
 F:228-289/Domain: immunoglobulin homology <IMM3>
 F:263-272/Region: NCAM binding #status predicted
 F:332-387/Domain: immunoglobulin homology <IMM4>
 F:419-481/Domain: immunoglobulin homology <IMM5>
 F:493-587/Domain: fibronectin type III repeat homology #status atypical <FN3>
 F:633-720/Domain: fibronectin type III repeat homology #status atypical <FN3>
 F:741-96/Region: fibronectin type III repeat homology #status predicted
 F:222,315,347,423,449,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 120; DB 1; Length 761;
 Best Local Similarity 22.2%; Pred. No. 0.065;
 Matches 61; Conservative 40; Mismatches 114; Indels 60; Gaps 11;
 QY 31 NNSIMLQTSK-----ENHALASSLCMDKQITONTYSKYLAEVNTSPVKAATNAV 81
 Db 171 NNYIQTIGIKKTDEGTGRCGRILARGEI-----NFKDIQVIVNVPPIQARQNTV 221
 QY 82 LCCPPIALRMILITWETIIIRGQPSCTKAYKETNETKETCTDERITWVSRRPDQSDIQ 141
 Db 222 NATANLQGSYIVLDAE-----GFPEPTMSWTKD-GEIIEBDEDEKIF---SDDSQILT 273
 QY 142 IRPVAITHDGYRCIMTPTDGNFRGVLHVLQVLTPEVTLFQNR-----TAVKAYA 194
 Db 274 IKKVDKNDSEAEYICIAENKAGEQDATHLKVFAKPIYVENQFAMELEBOVTLTCFA-S 332

QY 195 GKPAQISWIPREGDATKOEYWSNGTVYVSTCHMEVHNVSTV-----CHV 241
 Db 333 GDFPISITWSTNISTNISTSEKTLJDGHVVRSHA-----RVSSLTLSKIQYTDAGEYICTA 387
 QY 242 SHLTG--NKSLEYIELLPVPGAKSKAKUYIPIYILT 274
 Db 388 SNTIGDSQSWLYEVQYAP-----KLGQPVAVYT 416

RESULT 9

146591
 CD86 precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_rev: 14-Feb-1997 #text_change 23-Jul-1999
 C:Accession: U4691
 R:Isono, T.; Seto, A.
 Immunogenetics 42, 217-220, 1995
 A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
 A:Reference number: U4691; MUID:95369849; PMID:7642234
 A:Accession: U4691
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-330 <ISO>
 A:Cross-references: GB:D49842; NID:g755098; PIDN:BA08642.1; PID:g755099
 C:Superfamily: B7-2 antigen

Query Match 6.5%; Score 119.5; DB 2; Length 330;
 Best Local Similarity 22.6%; Pred. No. 0.026;
 Matches 77; Conservative 51; Mismatches 114; Indels 99; Gaps 18;
 QY 14 LITFLVLA-EAEGAAQPNNSIMLQTSKENHALASSLCMDKQITONTYSKYLAEVNTSW 72
 Db 9 LSVTFVFWALLLSGAA-----SLRQAYFNKTA---DLPC-----QFTNSQGRSISLVLVFW 57
 QY 73 PVKATNAVLCPPIALRLNLIITWETIIIRGQPSCTKAYKETNETKETCTDERITWVS 132
 Db 58 QDOER-----LVLYELFL-----GREKPDVNDPKYIGRTS 87
 QY 133 RPDQNSDQIRPVAITHDGYRCIMVTPDGNFRG-----YHQLVLT---PEV 178
 Db 88 PDQNSMQLQANVQIKKGYQCIV-----HRGAGLYPIYQMSLESLVIANFQPEI 141
 QY 179 TLFQNRNRTA---VCKAVAGP-AAQISWIPREGDATKOEYWSNGTVYVSTCHMEVH 233
 Db 142 TLINSTRNSAINLTCSVQGPPEPKKMFVLKTNKAT-TEY--DGYIEKQDNVTGLYN 198
 QY 234 VS-----TVCVSHLTGNKSLYIELLV-----PGAKSKAKUYIPIYILT 275
 Db 199 ISIGSTFSDIDINNAITVCLQ--TSTETYSQHPFIVRADPVPVPEKPLMLAAVALTL 256
 QY 276 ILTV-IVGFVWLK-----VNGCRKYKLNKTESPTVVE 307
 Db 257 IVVGIVLFLTMRKKEQCGVCECTIKKDKAENHVEE 297

RESULT 10
 A1054
 fasciadin II, transmembrane splice form precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 21-Apr-1992 #sequence_rev: 21-Apr-1992 #text_change 17-Mar-2000
 C:Accession: A41054
 R:Grenningloh, G.; Rehm, E.J.; Goodman, C.S.
 Cell 67, 45-57, 1991
 A:Title: Genetic analysis of growth cone guidance in Drosophila: fasciadin II functions
 A:Reference number: A41054; MUID:92005695; PMID:1913818
 A:Accession: A41054
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-811 <GR>
 A:Cross-references: GB:M77165; NID:g157402; PID:g157403
 C:Genetics:
 A:Gene: flyBase:Fa2
 A:Cross-references: flyBase:FBgn0000635

C:Superfamily: neural cell adhesion molecule, fibronectin type III repeat homology; immunoglobulin-like domain
C:Keywords: membrane protein

Query Match	6.3%;	Score 117;	DB 2;	Length 811;
Best Local Similarity	22.5%;	Pred. No. 0.12;		
Matches 69;	Conservative 40;	Mismatches 126;	Indels 72;	Gaps 14

```

QY      10 LGILLIITI-----FLVAEAGAAQPNISIMLTQTSKSNHALASSICMDENKQITQNS 62
Db      46 VGRPLITLCRPVPEPSIYADLQWMDNRNNTILPRKNGNQPPMYTEILPES----- 98
QY      63 KYLAENVNTPMYKMA-----TNVAVLCCPPIALRLMLITWEIIRGQ-PECTAYR 112
Db      99 --LALMTTSSVEMGKKYCTASVYANTEILEKGVITKIVYALITWNAENYPLPGDYV 156
QY     113 KETNETKENTCTBERITWVSRPD-----QNSDIQIRPAVITHDGYRRC--IMVT 159
Db     157 VMCEVKADPNPT--IDMLRNGDPRIRTNDKVVYQINGLLIRNVOESDEGIYTCRAVIE 213
QY     160 PDGNFHGHHLQVLYVPEV-----TLFQNRNRPAVCAYAGKPAQISITPBG---DC 209
Db     214 TGEILEETTRIVEVFIPDEILSLPTNIEAVEGKPRPANCIA-RGRVPEISWIRATQGLNV 272
QY     210 ATKOEYWSN--GIVTVKSTCHWEVANNSTVTCVSHLTG-----NKSLEYEL 254
Db     273 ATADRFQVNPQTGLVITISSVQ---DDVGYTYCLAKNRBAGVVDQTKRLNVLYRPQIY-EL 348
QY     255 LPVPGAK 261
Db     329 YNVTVGAR 335

```

RESULT 11

fasciclin II Pf-linked splice form precursor - fruit fly (Drosophila melanogaster)
 C|Species: Drosophila melanogaster
 C|Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 17-Mar-2000
 C|Accession: B41054
 R|Grenningloh, G.; Rehm, E.U.; Goodman, C.S.
 Cell 67, 45-57, 1991
 A|Title: Genetic analysis of growth cone guidance in Drosophila: fasciclin II functions
 A|Reference number: A41054; MUID:92005695; PMID:191818
 A|Accession: B41054
 A|Status: Preliminary
 A|Molecule type: mRNA
 A|Residues: 1-873 <GR>
 A|Cross-references: GB:M77166
 C|Genetics:
 A|Gene: FlyBase:Faaz2
 A|Cross-references: FlyBase:FBgn0000635
 A|Superfamily: neural cell adhesion molecule, fibronectin type III repeat homology; immunoglobulin-like domain
 A|Keywords: transmembrane protein

Query Match	6.3%;	Score 117;	DB 2;	Length 873;
Best Local Similarity	22.5%;	Pred. No. 0.14;		
Matches 69;	Conservative 40;	Mismatches 126;	Indels 72;	Gaps 14.

```

QY 10 LGLLLITIT-----FLVAEAGGAQPRNSLMQTSKHNHALASSLCLMDKQIQTNS 62
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 46 VGRPLILITCPFLVPEESLVADLQMDKDNRRNITLPPENRRQPPMYITTLGGS----- 98
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 KVLAEVNTSWPVCA-----TNALVCCPILRLIITWEILLRQQ-PSCKAYR 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 99 --LALMITSLSVMSGKYYCTASANTBELRGVITKIKYVALITTNAPENQYITLGDYV 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 KETNETKEINCTDERITWVSRPD-----QNSDLQIRPVAITHGDIYRC--IMVT 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 VMCEVAKADPRPT---IDMLRNDPIRTTNDKIVYQTNGLIRNQESDESDIYCPRAVIE 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 PDGNFTRGHYLOVLVPIEV-----TLFQNRNRAVCKAVAGGAQISIMIEG---DC 209
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 TGBELLETRIVFETDPEIISLPTMLEAVGGAPPAANTLA-RGKVPESIMIDATQVLN 272
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY	210	ATGQEWNSN---GTVVSKTCHEVYHNSVTCVAVSHLTG-----	NSKLYIEL	254
Db	273	ATADRRQVNPQGLVLTISVSQ---DDVGYTTCGLAKRRAGVVDQKTKLNTLVLRPQIY-EL		348
QY	255	LPVPGAK 261		
Db	329	YNTVIGAK 335		

RESULT 12
TICNT.

neural cell adhesion molecule long domain form precursor - chicken

N-Contents: neural cell adhesion molecule, short domain form (NCAM-140)
C-Species: Gallus gallus (chicken)
C-Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 22-Jun-1999
R-Crossing: A43613, B45613, A25435, B25435, A46550, S36550, A44369, A60852, S29668
R-Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Edelman, G.M.; Edelman, R.
Science 236, 799-806, 1987
A>Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, cell su
A-Accession: A43613
A-Reference number: A43613; MUID:87206190; PMID:3576199
A-Molecule type: mRNA
A-Residues: 1-175 <CU2>
A-Cross-references: GB:M15860
A-Accession: B43613
A-Molecule type: Protein
A-Residues: 20-44,120-127,202-221,320-342,399-415,640-659,822-828 <GUN>
A>Note: Asn-222 probably binds carbohydrate; Asn-226 probably does not
R-Hemperly, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.
Proc.Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986
A>Title: Sequence of a cDNA clone encoding the polystylic acid-rich and cytoplasmic dome
A-Reference number: A25435; MUID:86206089; PMID:3458261
A-Accession: A25435
A-Molecule type: mRNA
A-Residues: 128-1091 <HEM>
A-Cross-references: GB:M13210
A-Accession: B25435
A-Molecule type: Protein
A-Residues: 128-140,222-240,428-439,611-631,744-760,763-781,1080-1084 <HE2>
R-Murray, B.A.; Owens, G.C.; Prediger, E.A.; Crossen, K.L.; Cunningham, B.A.; Edelman,
J. Cell Biol. 103, 1431-1439, 1986
A>Title: Cell surface modulation of the neural cell adhesion molecule resulting from alth
A-Reference number: A46550; MUID:87033934; PMID:3771645
A-Accession: A46550
A-Molecule type: DNA
A-Residues: 810-1070 <NOR>
A-Cross-references: GB:X04479
R-Saenger, M.; Covault, J.
submitted to the EMBL Data Library, February 1993
A-Reference number: S36950
A-Accession: S36950
A-Molecule type: DNA
A-Residues: 1-17 <SAS>
A-Cross-references: EMBL:X070342; NID:g417631; PIDN:CAA49807.1; PID:g417632
R-Colwell, G.; Li, B.; Forrest, D.; Brackeumy, R.
Genetics 14, 875-882, 1992
A>Title: Conserved regulatory elements in the promoter region of the N-CAM gene.
A-Reference number: A44369; MUID:93122797; PMID:1478668
A-Accession: A44369
A-Molecule type: Protein
A-Residues: 1-17 <COR>
A-Cross-references: EMBL:Z12128; NID:g63653; PIDN:CAAT8113.1; PID:g63654
A-Experimental source: White Leghorn
R-Cole, G.U.; Loewy, A.; Cross, N.V.; Ateson, R.; Glaeser, L.
J. Cell Biol. 103, 1739-1744, 1986
A>Title: Topographic localization of the heparin-binding domain of the neural cell adhes
A-Reference number: A60852; MUID:87057627; PMID:2430978
A-Accession: A60852
A-Molecule type: Protein
A-Residues: 20-29 <COL>
R-Rao, Y.; Wu, X.F.; Gartley, U.; Rutishauser, U.; Siu, C.H.
J. Cell Biol. 118, 937-949, 1992

A>Title: Identification of a peptide sequence involved in homophilic binding in the neu
 A/Reference number: A4380, MUID:9233934, PMID:138002
 A/Comment: annotation; homophilic binding region
 C/Comment: NCM mediates cell-cell adhesion via homophilic binding with another NCM mol
 C/Superfamily: various forms of NCM are produced by alternative splicing.
 C/KeyWords: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C/KeyWords: alternative splicing; brain; cell adhesion; duplication; heparin binding; st
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-1091/Domain: product: neural cell adhesion molecule, long domain form #status experimental
 F:20-899,1071-1091/Domain: product: neural cell adhesion molecule, short domain form #status exp
 F:20-711/Domain: extracellular #status predicted <EXT>
 F:34-98/Domain: immunoglobulin homology <IM1>
 F:34-99/Domain: immunoglobulin homology <IM2>
 F:132-191/Domain: immunoglobulin homology <IM3>
 F:152-156/Region: heparin binding #status predicted
 F:161-165/Region: heparin binding #status predicted
 F:228-289/Domain: immunoglobulin homology <IM3>
 F:262-271/Region: NCM binding #status experimental
 F:322-387/Domain: immunoglobulin homology <IM4>
 F:419-481/Domain: immunoglobulin homology <IM5>
 F:518-595/Domain: fibronectin type III repeat homology <FN3A>
 F:624-685/Domain: fibronectin type III repeat homology <FN3B>
 F:712-729/Domain: transmembrane #status predicted <TM>
 F:730-1091/Domain: intracellular #status predicted <INT>
 F:41-96,113-189,235-287,328-385,426-479/Disulfide bonds: #status predicted
 F:122/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:315,347,423,449,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.3%; Score 117; DB 1; Length 1091;
 Best Local Similarity 22.6%; Pred. No. 0.18;
 Matches 64; Conservative 39; Mismatches 104; Indels 76; Gaps 12;

QY 31 NNSLMLOTST-----ENHALASSSLCMEKQITON-----YKVLAEVNTSP 73
 DB 171 NNYIQIRIGIKTDEGTGRCGRILARGEINFKDIOIVVPPSVARROSTMAATNLSSQ 230
 QY 74 VKKATNAVLCCEPIALRNLIITWEIILRGOPCTKAYRENETETETCTERTWTR 133
 DB 231 VTLACDADGPRP-----TMTW--TKQGEF-----IEQDNEEKSTNYD----- 268
 QY 134 PDNSDLQIRPVAITHDGYRCIMVTPDNGFHRGYHQLVLPTEVTLFQNRK----- 186
 DB 269 ---GSEILIKVYKSDAEYICIAENKAGEQDATHILKVFAPKPIYVNTKAMELEDOI 325
 QY 187 TAVCKAAKPAQKQISIPFGDCATKQEKWNGTVAVKSCHWEVNVSTV----- 238
 DB 326 TLTCEA-SGDFISITWKTSTNINSEKTLDRIVRSHA-----RVSLTLKEIQYTD 379
 QY 239 -----CHVSHLTG--NKSLEYIELLPVGAACKSAKLYIPYIILT 274
 DB 380 AGEVYCTASNTIGDQSQMYLEVOYAP-----KLQGPVAVYT 416

RESULT 13

RWHUPD
 poliovirus receptor splice form delta precursor - human
 N/Alternate names: poliovirus receptor H20B
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
 R/Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Itzuka, N.; Takeuchi, K.; Tak
 EMO J. 9, 3217-3224, 1990
 A/Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
 A/Reference number: S12048; MUID:91006015; PMID:2170108
 A/Accession: A43024
 A/Molecule type: DNA
 A/Residues: 1-392 <KO1>
 A/Cross-references: EMBL:X64116
 A/Note: 67-Ala was also found
 R/Mendelsohn, C.L.; Wimmer, E.; Racanelli, V.R.
 Cell 56, 855-865, 1989
 A/Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
 A/Reference number: A90910; MUID:89168426; PMID:2538245
 A/Accession: B31496

A/Molecule type: mRNA
 A/Residues: 1-66, 'A', 68-392 <MEN>
 A/Cross-references: GB:M24406
 C/Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
 C/Genetics:
 A/Gene: GDB:PVR; PVS
 A/Map position: 19q13.2-19q13.2
 A/Introns: 27/1; 143/1; 242/1; 281/2; 331/1
 C/Superfamily: poliovirus receptor; immunoglobulin homology
 C/KeyWords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pr
 F:1-20/Domain: signal sequence #status predicted <Sig>
 F:21-392/Domain: poliovirus receptor delta #status predicted <MAT>
 F:421-343/Domain: extracellular #status predicted <EXT>
 F:442-125/Domain: immunoglobulin homology <IM1>
 F:159-223/Domain: immunoglobulin homology <IM2>
 F:259-314/Domain: immunoglobulin homology <IM3>
 F:344-357/Domain: transmembrane #status predicted <TM>
 F:368-392/Domain: intracellular #status predicted <INT>
 F:49-123,166-221,266-312/Disulfide bonds: #status predicted
 F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 6.3%; Score 115.5; DB 1; Length 392;
 Best Local Similarity 24.4%; Pred. No. 0.069;
 Matches 59; Conservative 32; Mismatches 82; Indels 69; Gaps 11;

QY 71 SWPKATNAVLCCEPIALRNLIITWEIILRGOPCTKAYRENETETETCTERTWTR 98
 DB 8 AMPLIALLVLLSPMPGTDVVVQAPQVPGFGLGSVTLPCYLQVNMETVHVSQTLW- 66
 QY 99 IILRGOPCTKAYRENETETETCTERTWTRPDNSDLQIRPVAITHDGY 153
 DB 67 --THGSGMAVYHQVQGSYSKRLBEVVAIRLGEIR--NALSIRMGLRVEDGNY 121
 QY 154 RCIMVT-PDNGFHRGYHQLVLPTE-----VTLFQNRRTAVCKAAKPAQISWIP 205
 DB 122 TCLFVTFPGQSRSDVILRLVLAQKQNTAEVQKQLTGEPVPMARCVSTGCRPFAQITWHS 181
 QY 206 E-GDCATKQ-EYWSNQTVAVKSCHWEVNVSTV-----TTCVYSH-----LTGNS 249
 DB 182 DLGMPNTSQVPGSLGTVTSL--WILVPSQVQCKVYCKVHSEFKPQLITVNT 239
 QY 250 LY 251
 DB 240 VY 241

RESULT 14

RWHUPA
 poliovirus receptor splice form alpha precursor - human
 N/Alternate names: poliovirus receptor H20A
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 R/Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Itzuka, N.; Takeuchi, K.; Tak
 EMO J. 9, 3217-3224, 1990
 A/Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
 A/Reference number: S12048; MUID:91006015; PMID:2170108
 A/Accession: S12048
 A/Molecule type: DNA
 A/Residues: 1-417 <KO1>
 A/Cross-references: EMBL:X64116; NID:935809; PIN:CA45478.1; PID:9825708
 A/Note: 67-Ala was also found
 R/Mendelsohn, C.L.; Wimmer, E.; Racanelli, V.R.
 Cell 56, 855-865, 1989
 A/Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
 A/Reference number: A90910; MUID:89168426; PMID:2538245
 A/Accession: A31496
 A/Molecule type: mRNA
 A/Residues: 1-66, 'A', 68-417 <MEN>
 A/Cross-references: GB:M29535

C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f

C:Genetics:

A:Gene: GDB:PVR, PVS

A:Cross-references: GDB:120324; OMIM:173850

A:Map position: 19q13.2-19q13.2

A:Introns: 27/1, 143/1, 242/1, 281/2, 331/1, 384/1, 394/3

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pr

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>

F:21-343/Domain: extracellular #status predicted <EXT>

F:21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRA>

F:42-125/Domain: immunoglobulin homology <IM1>

F:159-223/Domain: immunoglobulin homology <IM2>

F:259-314/Domain: immunoglobulin homology <IM3>

F:344-367/Domain: transmembrane #status predicted <TM>

F:368-417/Domain: intracellular #status predicted <INT>

F:49-123,166-221,286-312/Dissulfide bonds: #status predicted

F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 6.3%; Score 115.5; DB 1; Length 417;

Best Local Similarity 24.4%; Pred. No. 0.074; Mismatches 82; Indels 69; Gaps 11;

Matches 59; Conservative 32; Mismatches 82; Indels 69; Gaps 11;

QY 71 SMPVCMATRAVLCPPALRNIT-----ITWE 98

DB 8 AMPLLLVALLVSWPPFGTGVVQAPVQVGLDSTVLPCLQVPMVEVTHVSOLTM- 66

QY 99 ILRGQSCSTKAYKET-----NETKENTCDERTITWRSDNSDQIRVATITHGXY 153

DB 67 --TRHGEGSMVAVFQTGPGSYSESKRLFFVAARIGALR--NALSMPGLRVDEGNY 121

QY 154 RCINVT-PDGNFHRGYLQVLTPE-----VTLFQNRNTRAVCKAVAGRAAQISMIP 205

DB 122 TCLFTFTFGQGSRVDIWIKVLAQPNTAEVQKVLGTGSPVMACVSTGGRPPAQITWHS 181

QY 206 E--GDCATKQ--EYNSGTVATKSTCHWEVHVS-----TYVCHVSH-----LTGNS 249

DB 182 DLGKPNTPSQVPGFLSGVTVTSL--WILPSSQVQDKNVCKVHESFEKRPQLLTVNT 239

QY 250 LY 251

DB 240 VY 241

RESULT 15

A:1060

neural cell adhesion molecule LI precursor - human

N:Alternate names: L1CAM

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jul-2000

C:Accession: A41060; S18454; A35331; S21971; S21972; A60223; A31072; G02506

R:HLavin, M.L.; Lemmon, V.

Genbank 11, 416-423, 1991

A:Title: Molecular structure and functional testing of human L1CAM: an interspecies comp

A:Reference number: A41060; MUID:92120663; PMID:1769655

A:Accession: A41060

A:Molecule type: mRNA

A:Residues: 1-1257 <HLA>

A:Cross-references: GB:M64296; NID:g186053; PIDN:AA014352.1; PID:g3068548

R:Kobayashi, M.; Mura, M.; Asou, H.; Uyemura, K.

Biochim. Biophys. Acta 1090, 236-240, 1991

A:Title: Molecular cloning of cell adhesion molecule LI from human nervous tissue: a com

A:Reference number: S18454; MUID:92031698; PMID:1932117

A:Accession: S18454

A:Molecule type: mRNA

A:Residues: 1-3, 'V', 5-215, 'T', 217-249, 'T', 251-275, 'SV', 278-356, 'E', 358-625, 'V', 627-1257

A:Cross-references: EMBL:X59647; NID:g55009; PIDN:CAA42508.1; PID:g55010

A:Notes: the authors translated the codon GAA for residue 27 as Gly

R:Djball, M.; Mattei, M.G.; Nguyen, C.; Roux, D.; Demengot, J.; Dentot, F.; Moos, M.;

Genomics 7, 587-593, 1990

A:Title: The gene encoding L1, a neural adhesion molecule of the immunoglobulin family,

A:Reference number: A35331; MUID:90353557; PMID:2387585

A:Accession: A35331

A:Molecule type: DNA

A:Residues: 332-371 <DNA>

A:Cross-references: GB:M55271

R:Rosenthal, A.; Mackinnon, R.N.; Jones, D.S.C.

Nucleic Acids Res. 19, 5395-5401, 1991

A:Title: PCR walking from microdissection clones M54 identifies three exons from the hum

A:Reference number: S21971; MUID:92020233; PMID:1523824

A:Accession: S21971

A:Molecule type: DNA

A:Residues: 1082-1176 <ROS>

A:Cross-references: EMBL:X58775; NID:g29642; PIDN:CAA41576.1; PID:g29643

A:Accession: S21972

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 353-935, 'V', 937-1176 <RO2>

A:Cross-references: EMBL:X58776; NID:g29644; PIDN:CAA37831.1; PID:g4467833

R:Harper, J.R.; Prince, J.T.; Healy, P.A.; Stuart, J.K.; Nauman, S.J.; Stallcup, W.B.

J. Neurochem. 56, 797-804, 1991

A:Title: Isolation and sequence of partial cDNA clones of human L1: homology of human a

A:Reference number: A60223; MUID:91132183; PMID:193895

A:Accession: A60223

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1030-1115, 'WLC', 1118-1176, 1181-1257 <HAR>

R:Wolfe, J.M.; Frank, R.; Mujico, K.; Spiro, R.C.; Reisfeld, R.A.; Rathjen, F.G.

J. Biol. Chem. 263, 11943-11947, 1988

A:Title: A human brain glycoprotein related to the mouse cell adhesion molecule L1.

A:Reference number: A31072; MUID:88298876; PMID:3136168

A:Accession: A31072

A:Molecule type: protein

A:Residues: 'Q', 21-36 <WOL>

R:Platzer, M.; Bauer, D.; Drescher, B.

submitted to the EMBL Data Library, March 1995

A:Reference number: H01368

A:Accession: G02506

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1257 <PLA>

A:Cross-references: EMBL:U52112; NID:g1302657; PIDN:AA01746.1; PID:g1302658

C:Genetics:

A:Gene: GDB:L1CAM

A:Cross-references: GDB:120133; OMIM:303350; OMIM:308840

A:Map position: Xq28-Xq28

A:Introns: 26/1, 31/1, 66/2, 134/1, 175/1, 232/1, 265/2, 331/1, 375/1, 423/1, 460/2; 514

2

C:Superfamily: neural cell adhesion molecule LI; fibronectin type III repeat homology;

C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; transmembr

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-1257/Product: neural cell adhesion molecule LI #status predicted <MNT>

F:257-314/Domain: immunoglobulin homology <IM1>

F:352-593/Domain: immunoglobulin homology <IM2>

Query Match 6.2%; Score 115; DB 1; Length 1257;

Best Local Similarity 20.1%; Pred. No. 0.31; Mismatches 135; Indels 72; Gaps 11;

Matches 64; Conservative 47; Mismatches 135; Indels 72; Gaps 11;

QY 77 ATNAVCCPP-----IALRNLIITWEILRQSPCTAKRKETMETKNTCT 124

DB 231 ATNSKIDRKPRLLFPNSSSHVLAQGPV-L-ECTABFPPTTKMLRPSGMPA---- 285

QY 125 DEBITVSRPDQNSDQIRPVAITHDGYRCIMVTPDGNFHRGYLQV-----LVTPEV 178

DB 286 -DRVTV--QNNKKTLLQKVGEDDEGEYRCIAENSIGSARHAYTVTAAPYWLHKPQS 341

QY 179 TLFQNRNTRAVCKAVAGRAAQISW-----IPGDCATKREYNSNGVTVKSTCHWEVNV 234

DB 342 HLYGPESTARLDCQVGRQPEPTWINGIPVEELAKQDKYRIQGCALLTSVQPSDTNV 401

QY 235 STYTCVSH--LTGNSKLYIELLPVGAKKSAKLYI-----PYILITITITIVGIWL 286

DB 402 TQCEANRNGILLANAYITVQLPKILRADNQTMVAVGSTRAYLLCKAFGAPVSVQVL 461

Fri May 7 11:49:15 2004

us-10-009-445a-20.rpr

Page 8

QY	287	LKNGCRKYLKNTSTPVEDEMOFYASYT-----	EKNPLTD	326
Db	462	-----DGDGTTVLQDERFFPYANGTIGIRDLOANDIGRYFCIAANDQNNVTIM		509
QY	327	TTNKVK-ASQALQSEVDT		343
Db	510	ANLKVXDATQITQGPST		527

Search completed: May 7, 2004, 11:42:44
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 11:35:54 ; Search time 17 Seconds

(without alignments)
1065.907 Million cell updates/sec

Title: US-10-009-445a-20

Perfect score: 1846
Sequence: 1 MLCFWRANGLILITLFL.....NKYASQALQSDVDTLTL 348

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1706.5	92.4	325	1	MOXR_HUMAN
2	911	49.3	327	1	MOXR_RAT
3	899.5	48.7	326	1	MOXR_MOUSE
4	125.5	6.8	530	1	PVR2_MOUSE
5	125.5	6.8	538	1	PVR2_HUMAN
6	122.5	6.6	524	1	BUTY_MOUSE
7	122.5	6.6	853	1	NCA1_BOVIN
8	120	6.5	761	1	NCA2_HUMAN
9	120	6.5	848	1	NCA1_HUMAN
10	119.5	6.5	330	1	CD86_RABIT
11	117	6.3	873	1	PAS2_DROME
12	117	6.3	1091	1	NCA1_CHICK
13	115.5	6.3	417	1	PVR_HUMAN
14	115	6.2	1257	1	CAML_HUMAN
15	114.5	6.2	858	1	NCA1_RAT
16	112	6.1	515	1	PVR1_MOUSE
17	110.5	6.0	725	1	NCA2_MOUSE
18	110.5	6.0	1115	1	NCA1_MOUSE
19	108.5	5.9	517	1	PVR1_HUMAN
20	108.5	5.9	564	1	CL66_BRARE
21	108	5.9	496	1	ACH3_CHICK
22	105.5	5.7	417	1	PVR_CERAE
23	105.5	5.7	515	1	PVR1_PIG
24	105.5	5.7	1070	1	PTK7_HUMAN
25	105	5.7	837	1	NCA2_HUMAN
26	103.5	5.6	271	1	OX2V_KSHV
27	103.5	5.6	378	1	OX2G_MOUSE
28	103.5	5.6	332	1	CD22_MOUSE
29	102.5	5.6	278	1	OX2G_HUMAN
30	101.5	5.5	526	1	BUTY_HUMAN
31	101.5	5.5	686	1	IFL2_MOUSE
32	101.5	5.5	1461	1	NBO1_HUMAN
33	101	5.5	332	1	CD22_PANTR

34	101	5.5	1051	1	PTK7_CHICK	Q91048 gallus gall
35	100.5	5.4	332	1	CD22_GORGO	Q91048 gorilla gor
36	100	5.4	821	1	FCR2_HUMAN	Q21802 homo sapien
37	99	5.4	862	1	CD22_MOUSE	P35329 mus musculu
38	98.5	5.3	345	1	OPCM_BOVIN	P18343 bos taurus
39	98	5.3	278	1	OX2G_RAT	P04318 rattus norv
40	98	5.3	1259	1	CAML_RAT	Q05695 rattus norv
41	97.5	5.3	345	1	OPCM_HUMAN	Q14582 homo sapien
42	97.5	5.3	682	1	TD85_HUMAN	Q8nat2 homo sapien
43	97.5	5.3	1260	1	CAML_MOUSE	P1627 mus musculu
44	97.5	5.3	1447	1	DCC_MOUSE	P70211 mus musculu
45	97	5.3	348	1	KIRO_RAT	Q920f8 rattus norv

ALIGNMENTS

```

RESULT 1
ID      MOXR_HUMAN      STANDARD; PRT; 325 AA.
AC      Q8TD46; Q8TD44; Q8TD45; Q8TD52;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Cell surface glycoprotein OX2 receptor precursor (CD200 cell surface
DE      glycoprotein receptor).
GN      MOXR OR OXR OR CD200R OR CTR2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RA      Wright G.J., Brown M.H., Barclay N.;
RT      "X14, the HIV-8 viral OX2 homolog interacts with the human OX2
RT      receptor with identical affinity and kinetics as the host OX2
RT      protein."
RL      Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RA      Suarez A., Viettes J.M., De la Torre R., Ortega M.A., Gil A.,
RA      Sanchez-Pozo A.;
RT      "Characterization of human CD200R gene."
RL      Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: Receptor for the OX2 cell surface glycoprotein. Also
CC      binds to HIV-8 X14 viral OX2 homolog with identical affinity and
CC      kinetics as the host OX2.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1 and 4);
CC      secreted (isoform 2 and 3).
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Name=1;
CC      IsoId=Q8TD46-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q8TD46-2; Sequence=VSP_002614, VSP_002615, VSP_002616;
CC      Name=3;
CC      IsoId=Q8TD46-3; Sequence=VSP_002615, VSP_002616;
CC      Name=4;
CC      IsoId=Q8TD46-4; Sequence=VSP_002614;
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC      This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
DR      EMBL; AF283760; AAN61171.1; -
DR      EMBL; AF497548; AAM15157.1; -
DR      EMBL; AF497549; AAM15158.1; -

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DR	EMBL; AF497550; AAM16159.1; -
DR	EMBL; AF495380; AAM14622.1; -
DR	MIM; 607546; -
DR	InfePro; IPRO07110; IG-like.
DR	Prosites; PSS0835; IG_Like; 1.
KM	Transmembrane Receptor; Glycoprotein; Signal; Polymorphism;
KM	Alternative splicing.
FT	SIGNAL
FT	1
FT	CHAIN
FT	29
FT	DOMAIN
FT	29
FT	TRANSMEM
FT	244
FT	DOMAIN
FT	265
FT	DOMAIN
FT	53
FT	DOMAIN
FT	140
FT	DISULFID
FT	60
FT	167
FT	CARBOHYD
FT	37
FT	CARBOHYD
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FT	99
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FT	325
FT	VARSPPLIC
FT	89
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FT	VARIANT
FT	121
FT	121
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FT	177
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SEQ	325 AA; 36620 MM; DDFP4BIF6S37BBD CRC64;

Query Match	Similarity	92.4%	Score 1706.5	DB 1	Length 325
Best local	93.1%	Pred: No. 6.3e-140			
Matches 324	Conservative 1	Mismatches 0	Indels 23	Gaps 1	
QY	1	MLCPWRANLGLILLITLFLVAEAGAAQPNNSLMLQTSKENHALASSSLCMEDEKQITON	60		
Db	1	MLCPWRANLGLILLITLFLVA-----ASSSLCMEDEKQITON	37		
QY	61	YSKVLAEVNTSPVYKATNAVLCCEPIALRLIIITTWELILRGDPSCTRAYKENETPE	120		
Db	38	YSKVLAEVNTSPVYKATNAVLCCEPIALRLIIITTWELILRGDPSCTRAYKENETPE	97		
QY	121	TNCTDERITWVRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLTVPETVL	180		
Db	98	TNCTDERITWVRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLTVPETVL	157		
QY	161	FONRRRTAVCKVAVKRPAAQISWIEBGDCAITQWMSNGTVYKSTCMHEVNVSTWCH	240		
Db	158	FONRRRTAVCKVAVKRPAAQISWIEBGDCAITQWMSNGTVYKSTCMHEVNVSTWCH	217		
QY	241	VSHTLGNKSLYIELLPVPGAKKSAAKLYIPYIIITLITLITVGFIMLLKVNCGRKTKLNT	300		
Db	218	VSHTLGNKSLYIELLPVPGAKKSAAKLYIPYIIITLITLITVGFIMLLKVNCGRKTKLNT	277		
QY	301	ESTPVAVEEDBMOPVASYTEKKNPLVDITTKVAKSQAQLQSEVDTDLHTL	348		
Db	278	ESTPVAVEEDBMOPVASYTEKKNPLVDITTKVAKSQAQLQSEVDTDLHTL	325		

	Dt	28-FEB-2003	(Rel.	.41,	Created)	
	Pt	28-FEB-2003	(Rel.	.41,	Last sequence update)	
	Pt	10-OCT-2003	(Rel.	.42,	Last annotation update)	
	Dc	Ox102 antigen				
	Dc	Glycoprotein receptor				
	Dc	Cox2r Or Ox2r				
	Dc	Rattus norvegicus (Rat).				
	Dc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Dc	Mammalia; Euarchontia; Rodentia; Sciurognathi; Muridae; Rattus.				
	Dc	[NCBI_Taxid=10116]				
	Dc	SEQUENCE FROM N.A., SEQUENCE OF 24-42, CHARACTERIZATION, AND TISSUE SPECIFICITY.				
	Dc	STRAIN-PVG:				
	Dc	MEDLINE=20431845; PubMed=10981966;				
	Dc	Wright G.J., Pulkavac M.T., Willis A.C., Hoek R.M., Sedgwick J.D., Brown M.H., Barclay A.N.;				
	Dc	"myeloid/neuronal cell surface OX2 glycoprotein recognizes a novel receptor on macrophages implicated in the control of their function."				
	Dc	Immunoty 13:333-242(2000).				
	Dc	- FUNCTION: Receptor for the OX2 cell surface glycoprotein.				
	Dc	- SUBCELLULAR LOCATION: Type I membrane protein.				
	Dc	- TISSUE SPECIFICITY: Restricted to cells of the myeloid lineage.				
	Dc	- PTM: Phosphorylated on tyrosine residues.				
	Dc	- PMT: Highly N-glycosylated.				
	Dc	- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.				
	Dc	- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.				
	Dc	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isdb.ch/announce/ or send an email to license@isdb-sib.ch).				
	Dc	EMBL; AF231392; AAF98555.1; .				
	Dc	InterPro; IPRO07110; Ig-Like.				
	Dc	InterPro; IPR003599; Ig.				
	Dc	SMART; SMO0409; IG_1.				
	Dc	PROSITE; PS50833; IG_LIKE; 2.				
	Dc	TraNsmembrane; Receptor; Glycoprotein; Signal; Phosphorylation; Antigen.				
	Dc	SIGNAL				
	Ft	CHAIN	24	327		
	Ft	DOMAIN	24	239		
	Ft	TRANSMEM	240	260		
	Ft	DOMAIN	261	327		
	Ft	DOMAIN	26	145		
	Ft	DOMAIN	147	226		
	Ft	DISULFID	58	129		
	Ft	DISULFID	164	213		
	Ft	CARBOND	29	29		
	Ft	CARBOND	34	34		
	Ft	CARBOND	43	43		
	Ft	CARBOND	96	96		
	Ft	CARBOND	159	159		
	Ft	CARBOND	187	187		
	Ft	CARBOND	192	192		
	Ft	CARBOND	222	222		
	Ft	SEQUENCE	327 AA;	35533 MW;	BK067FFC77B610C CRC64;	
	Qy	Query Match	49.3%;	Score 911;	DB 1;	Length 327;
	Db	Best Local Similarity	53.7%;	Pred. No. 2.9e-71;		
	Matches	188;	Conservative % 40;	Mismatches 92;	Indels 30;	Gaps 4;
	Yq	YSKYIAEVNTSWPVMAATNAVLCCPPIALRNLLIITWEILLRGPSCKTKRKETNETKE MLCEWRIRSHVAALLIWGF-----AASSCPDNQTMON				60
	Yq	61 YSKYLAEVNTSWPVMAATNAVLCCPPIALRNLLIITWEILLRGPSCKTKRKETNETKE MLCEWRIRSHVAALLIWGF-----AASSCPDNQTMON				120
	Nd	NSNMTEVTNVTFVMGKKALKCCPSISLTAVLIITWTTLTRGGPCSIISKADRTREHE				94

GN PVRI2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racanelli V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene."
RL J. Virol. 66:12807-2813(1992).
RN (2)
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nemoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus."
RL J. Biol. Chem. 269:8431-8438(1994).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=223828257; PubMed=12477932;
RA Strausberg R., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Scheffer C.F., Bhat N.K.,
RA Altchul S.F., Zeeberg B., Buewer K.R., Schaefer C.F., Hsieh P.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachleon M., Soares M.B., Bonaldi M.P., Caavaent T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shvachenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (4)
RP CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racanelli V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEb)
RT mediates entry of pseudotables virus but not herpes simplex virus
RT types 1 and 2."
RL J. Virol. 73:4493-4497(1999).
RN (5)
RP FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY
INTO CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P33507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P33507-2; Sequence=VSP_002630, VSP_002631;
CC -1- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC	EMBL; M80206; AAA39734.1; -
DR	EMBL; D26107; BAA05103.1; -
DR	EMBL; BC059941; AAH59941.1; --
DR	PIR; A38211; HUMSP3.
DR	PIR; A53437; A53437.
DR	MED; MG197822; PVAL12.
DR	InterPro; IPR007110; IG_1like.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; IG; 3.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PSS0835; IG_Like; 3.
KW	Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW	Repeat, Alternative splicing.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	VARSPLIC
FT	VARSPPLIC
FT	SEQUENCE
FT	SEQ
FT	Query Match
FT	Best Local Similarity
FT	Matches
FT	Match
FT	63 KYLAENVTSMPVKATNAVLCC--PIVALNLIIITWE-----ILLGDSCTKAYRKE 114
FT	DB 37 RVLEVANG---RLGGIVELPCHLLPTTER-VQVTWMQRDGVVAHFHPSFGVD--- 88
FT	OY 115 TNETKENNCTDERITWT-SRPDQNSLDQ----IRPVALITHDGYYRCIMWT-PQGNFHKG 167
FT	DB 89 ---PNSQFSKDRIISFYRARARETNADLRDTLAFRGVRVEDEGNYTCFAFFENGTRRGV 144
FT	OY 168 YHLQVLTWP-----EVTLFQNNRNRAVCAVKGAPDAQISWIPE-GDCATKQEWV-S 217
FT	DB 145 TWLVAVINGPENHAHAGQEVTTIGPGVAVAACVSTGRRPARITWTISSLGAEAKDIOEPGIQ 204
FT	OY 218 NGTLYTKASTCHEVHNVS-----TVTGHVSHLTGKNKLYIELLV 257
FT	DB 205 AGTVTIIS-RYSILVPVGADGVKRVKVEHESEFEPI---LLRV 244
FT	RESULT 5
FT	ID_PVR2_HUMAN STANDARD: PRT; 538 AA.
FT	AC Q92692; C75455; Q96J29;
FT	DT 16-OCT-2001 (Rel. 40, Created)
FT	DT 16-OCT-2001 (Rel. 40, Last sequence update)
FT	DT 10-OCT-2003 (Rel. 42, Last annotation update)
FT	DE Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (Hvrb) (Nectin 2) (CD112 antigen).
FT	DE PVR2 OR PRR2 OR HVRB.
FT	OS Homo sapiens (Human).
FT	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CC NCBI_TaxId=9606;
 CC [1]
 CC SEQUENCE FROM N.A. (ISOFORM DELTA).
 CC MEDLINE=95347610; PubMed=7622062;
 CC Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.,
 CC "The human PR2 gene, related to the human poliovirus receptor gene
 CC (PVR), is the true homolog of the murine MPH gene.";
 CC Gene 159:267-272(1995).
 CC [2]
 CC SEQUENCE FROM N.A. (ISOFORM ALPHA).
 CC MEDLINE=96921161; PubMed=9657005;
 CC Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
 CC Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.,
 CC A cell surface protein with herpesvirus entry activity (HvE) confers
 CC susceptibility to infection by mutants of herpes simplex virus type
 CC 1, herpes simplex virus type 2, and pseudorabies virus.";
 CC Virology 246:179-189(1998).
 CC [3]
 CC SEQUENCE FROM N.A. (ISOFORM ALPHA).
 CC TISSUE=Brain;
 CC MEDLINE=22386257; PubMed=12477932;
 CC Strausberg R.V., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hatleh F.,
 CC Diatchenko L., Marziani K., Farmer A.A., Rubin G.J., Hsieh F.,
 CC Stepien M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 CC Brownstein W.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.J.,
 CC Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 CC Bosak S.A., McWeen P.J., McKernan K.J., Malek J.A., Gamarallu P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 CC Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,
 CC Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 CC Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 CC "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [4]
 CC SEQUENCE OF 31-538 FROM N.A.
 CC Yoshituna K., Murray J.C.,
 CC "A transcriptional map in the region of 19q13 derived using direct
 CC sequencing and exon trapping.";
 CC Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC [5]
 CC SEQUENCE OF 449-538 FROM N.A.
 CC MEDLINE=99449047; PubMed=10520737;
 CC Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
 CC Ashworth L.K., Van Bockmeier P.M., Dawkins R.L.,
 CC "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
 CC PEREC1.";
 CC RL
 CC RL DNA Seq. 9:89-101(1998).
 CC -1- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND
 CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Delta;
 CC IsoId=Q92692-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -1- DATABASE: NAME=PROV; NOTE=PROV 1.74-77(2000).
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/204270028_g.htm".
 CC
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RESULT 6
BUTY MOUSE
ID BUTY_MOUSE STANDARD; PRT; 524 AA.
AC 062556; P97392;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).
GN BTN1A1 OR BTN.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=97148936; PubMed=8955761;
RA Ogg S.L., Komaragiri M.V.S., Mather I.H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophilin gene.";
RL Mamm. Genome 7:900-905 (1996).
RN [2]
RP SEQUENCE OF 39-487 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96125722; PubMed=8541302;
RA Ichii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT specifically associates with a 150-kDa protein of mammary epithelial
RT cells and milk fat globule membrane.";
RL Biochim. Biophys. Acta 1245:285-292 (1995).
CC -1- FUNCTION: May function in the secretion of milk-fat droplets. It
CC may act as a specific membrane-associated receptor for the
CC association of cytoplasmic droplets with the apical plasma
CC membrane (by similarity).
CC -1- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in
CC association with the milk-fat-globule membrane during lactation.
CC -1- DEVELOPMENTAL STAGE: Expression increases during the last half of
CC pregnancy and is maximal during lactation.
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
CC family.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC
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CC
DR EMBL; U67065; AAB51034.1; -
DR EMBL; S80642; AAB55893.1; -
DR MGD; MGI:103116; Bm1a1.1; -
DR InterPro; IPR001870; B502.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR005966; IG V.
DR InterPro; IPR006574; PRV.
DR InterPro; IPR003877; SPRV_receptor.
DR Pfam; PF00047; IG_1.
DR Pfam; PF00623; SPRV_1.
DR SMART; SM00406; IGv_1.
DR SMART; SM00589; PRV_1.
DR SMART; SM00449; SPRV_1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Transmembrane; Glycoprotein; 1.
KW Immunoglobulin domain; Signal; Repeat.
FT SIGNAL 1 26
FT CHAIN 27 524 BUTYROPHILIN.
FT DOMAIN 27 247 BUTYROPHILIN.
FT TRANSMEM 248 268 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 269 524 POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 29 141 IG-LIKE V-TYPE 1.
FT DOMAIN 149 235 IG-LIKE V-TYPE 2.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 46 46 D -> DD (IN REF. 2).
FT CONFLICT 117 117 V -> F (IN REF. 2).
FT CONFLICT 191 191 E -> D (IN REF. 2).
FT CONFLICT 210 210 R -> S (IN REF. 2).
FT CONFLICT 363 363 R -> E (IN REF. 2).
FT CONFLICT 408 408 T -> K (IN REF. 2).
FT CONFLICT 413 414 SL -> FF (IN REF. 2).
FT CONFLICT 420 423 PRRV -> LAEY (IN REF. 2).
FT CONFLICT 492 509 DIPSPREGCTSGDKDT -> GHSIVPAGRLVFMQRH
FT SEQUENCE 524 AA; 58406 MW; 333FDE2C7704480 CRC64;
SQ
Query Match 6.6%; Score 122.5; DB 1; Length 524;
Best Local Similarity 19.0%; Pred. No. 0.006;
Matches 73; Conservative 59; Mismatches 155; Indels 97; Gaps 15;
QY 1 MLCPRTRANIGLLILITFLVAEAGAGPNNISMLDTSKENALASSSLCMDEKOTON 60
DB 1 MAVPTNSCLVCLTTLVQLPLTDSA-----PDTYAP 35
QY 61 YSKVLAENVTSWPFVQATNAVLCC--PPIALRNLIITWEIIRGQPSCTKAYRKETNET 118
DB 36 QEPYALV-----GSDAELTGFSPNMSSEYEMELW--FRQTRSTAVLVYRDGOEQ 84
QY 119 KEINCTBER---ITWSRPDQNSDLOIRYVALTHGTYRCINWTPDGNHRYGLQVLY 174
DB 85 EGQDMTYRGRATLATAGLDDGRATLIRVRSDDQSEYRCLEFNDPFEAAVLYLVAA 144
QY 175 T--PEV--TLFQNRNRTAYCAVAKPAQISV-----IPGDCATRGQYVNSGTVT 222
DB 145 VGSDPQISMVQENGEHLETSQWPEPQVQRTGNREMLP--STSESKHNEBELFT 202
QY 223 VKSTCHWEHNAVSTVTCVSHLTKNSLYIEL-LPVGAKKSKALYPIYLITLITIV 281
DB 203 VAVSMTRDSIRKMSCCIONILGQKEVEISLPAPVFR---LTPWIVAVAILIAL 258
QY 282 GFI-----W-----LKVNGCRKYKTKSTEVVEDEMOFY 314
DB 259 GFLITGSIFFTWKLYKRSRKKEFGSKERLLBELNCKTVLHEVDV--LDPDTAHPH 316
QY 315 ASYTEKNNPLDYTTNNKYASQALQ 338
DB 317 LF-----LYEDSKSVRLSDSRQ 333
RESULT 7
NCBI_BOVIN STANDARD; PRT; 853 AA.
ID NCBI_BOVIN
AC P31836;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neutral cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain cortex.
RX MEDLINE=89378239; PubMed=2776887;
RA Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,
RA Petukhova G.V., Rakhitina T.V., Feshchenko B.A., Ishchenko K.A.,
RA Mirzoeva S.F., Chernova N.N., Dranysheva S.M.,
RT "Calcmodulin-independent bovine brain adenylate cyclase. Amino acid
RT sequence and nucleotide sequence of the corresponding cDNA."

RL FEBS Lett. 254:69-73(1989).
 RN [2]
 RX SEQUENCE OF 20-36.
 RX MEDLINE=86140120; PubMed=3512556;
 RA Rougon G., Marshak D.R.;
 RA "Structural and immunological characterization of the amino-terminal
 RT domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401(1986).
 RP [3]
 RP IDENTIFICATION AS N-CAM.
 RP MEDLINE=92111748; PubMed=1765159;
 RA Premont R.T.;
 RA "A bovine brain cDNA purported to encode calmodulin-insensitive
 RT adenylyl cyclase has extensive identity with neural cell adhesion
 RT molecules (N-CAMs)."
 RL FEBS Lett. 295:230-231(1991).
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
 CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
 CC neurites, etc.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing: Named isoforms=1;
 CC Comment=4 number of isoforms are produced;
 CC Name=1;
 CC -1- IsoId=P31836-1; Sequence=Displayed;
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- CAUTION: Was originally (Ref.1) thought to be a calmodulin-
 CC independent adenylylase cyclase.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, X16451; CAA34470.1; -
 CC DR PIR, A32976; IJBONC.
 CC DR HSSP, P40189; IJBONC.
 CC DR InterPro: IPR008957; FN III-like.
 CC DR InterPro: IPR003961; FN III.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR InterPro: IPR003598; Ig-C2.
 CC DR Pfam, PF00041; fn3; 2.
 CC DR Pfam, PF00047; Ig; 5.
 CC DR SMART, SM00060; FN3; 2.
 CC DR SMART, SM00408; IGC2; 5.
 CC DR PROSITE, PSS0835; IG-Like; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternative splicing; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 853
 FT FT
 FT DOMAIN 20 719
 FT TRANSMEM 720 737
 FT DOMAIN 738 853
 FT FT
 FT DOMAIN 20 111
 FT DOMAIN 116 205
 FT DOMAIN 212 300
 FT DOMAIN 307 412
 FT DOMAIN 415 500
 FT DOMAIN 527 604
 FT DOMAIN 633 700
 FT DOMAIN 152 166
 FT DOMAIN 161 165
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 266
 FT DISULFID 328 394
 FT DISULFID 435 488
 FT CARBOHYD 222 222

FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 487 487 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 93893 MW; 512FD49231A7A568 CRC64;
 Query Match 6.6%; Score 122.5; DB 1; Length 853;
 Best Local Similarity 22.2%; Pred. No. 0.011;
 Matches 65; Conservative 39; Mismatches 102; Indels 87; Gaps 13;
 QY 31 NNSIMLQTSK-----ENHALASSLCMDKQITON-----YSKVLAEVNTSWP 73
 Db 171 NNYLQIRGIKKTDEGTGRCGRILARGEINFKDIQIVVPPYQARQSVNATNLGQS 230
 QY 74 VKMATAVLCPPPIALNLIITWELLNGQPSCTAYRKEIETETNCTDERITWVR 133
 Db 231 VTLVCA-----EGRFPTVSWTKGQITE--NEDEKYL F-- 264
 QY 134 PDQNSDLQIRPVAITHDGYRCIMVTPDGNFRGYNLQVLTPEVTLFQNRNE----- 186
 Db 265 SDSSSELTIRKVDKNDAEYVICAENKAGQDASIHAKFAKRTIYVENQTA MELEGV 324
 QY 187 TAVCKAVAGRPAAQISWIPSGDCATQOE--YNS-----NGTVYKSCHEVNVST 236
 Db 325 TLNCEA-SGDPISITWRSTRNISSEKASWTRPEKQETLDDHMVVRSHA-----RVSS 378
 QY 237 VT-----CHVSLTG--NKSLEYELPPGAKKAKLYPIYILT 274
 Db 379 LTLKSLQYTDAGRYVCTASNTIGDSQSYLVEQVNP-----KLGGPVAVYT 425
 RESULT 8
 NCAL HUMAN
 ID NCAL2 HUMAN STANDARD; PRT; 761 AA.
 AC P13592; P13593;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
 DE (NCAM-120) (CD56 antigen).
 OS NCAM1 OR NCAM.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM N-CAM 120).
 RP TISSUE=Skeletal muscle;
 RC MEDLINE=89305258; PubMed=3251057;
 RA Barton C.H., Dickson G., Gower H.J., Rowett L.H., Putt W.,
 RA Elsom V., Moore S.E., Goridis C., Walsh F.S.;
 RA "Complete sequence and in vitro expression of a tissue-specific
 RT phosphatidylinositol-linked N-CAM isoform from skeletal muscle";
 RL Development 104:165-173(1988).
 RN [2]
 RP SEQUENCE OF 491-761 FROM N.A. (ISOFORM N-CAM 120).
 RP TISSUE=Skeletal muscle;
 RC MEDLINE=87301755; PubMed=2687295;
 RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
 RA Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
 RA "Human muscle neural cell adhesion molecule (N-CAM): identification
 RT of a muscle-specific sequence in the extracellular domain";
 RL Cell 50:1119-1130(1987).
 RN [3]
 RP SEQUENCE OF 491-655 FROM N.A. (ISOFORM C).
 RP MEDLINE=89077552; PubMed=3203385;
 RA Gower H.U., Barton C.H., Elsom V.L., Thompson J., Moore S.E.,
 RA Dickson G., Walsh F.S.;
 RA "Alternative splicing generates a secreted form of N-CAM in muscle
 RT and brain";
 RL Cell 55:955-964(1988).
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in

CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
 CC neurites, etc.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 120;
 CC IsoId=P13592-2; Sequence=Displayed;
 CC Name=N-CAM 140;
 CC IsoId=P13591-1; Sequence=External;
 CC Name=C; Synonyms=Secreted;
 CC IsoId=P13592-1; Sequence=VSP_002587;
 CC -1- SIMILARITY: Contains 5 Immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 Fibronectin type III domains.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CDS6 entry.
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cds6.htm".
 CC -----
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 CC -----
 DR EMBL; X16841; CA34739.1; -;
 DR EMBL; M17409; AAAS912.1; -;
 DR EMBL; M22094; AAAS910.1; -;
 DR EMBL; M22092; AAAS911.1; -;
 DR EMBL; M22091; AAAS911.1; JOINED.
 DR PIR; A31635; A31635.
 DR PIR; S07784; IJHUNG.
 DR Genew; HGNC:7656; NCAM1.
 DR MTW; 116930; -;
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:Plasma membrane; TAS.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; IG_II-like.
 DR InterPro; IPR003588; IG_C2.
 DR Pfam; PF00041; FN3; 2.
 DR Pfam; PF00047; IG; 5.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IG_C2; 5.
 DR PROSITE; PSS0835; IG_LIKE; 5.
 KM Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 KM GPI-anchor; Alternative splicing.
 FT SIGNAL
 FT 1
 FT CHAIN
 FT 20 761
 FT 19
 FT DOMAIN
 FT 20 111
 FT DOMAIN
 FT 116 205
 FT DOMAIN
 FT 212 301
 FT DOMAIN
 FT 308 403
 FT DOMAIN
 FT 406 491
 FT DOMAIN
 FT 518 595
 FT DOMAIN
 FT 660 727
 FT DISULFID
 FT 41 96
 FT DISULFID
 FT 139 189
 FT DISULFID
 FT 235 287
 FT DISULFID
 FT 329 385
 FT DISULFID
 FT 426 479
 FT CARBOHYD
 FT 222 222
 FT CARBOHYD
 FT 315 315
 FT CARBOHYD
 FT 347 347
 FT CARBOHYD
 FT 423 423
 FT CARBOHYD
 FT 449 449
 FT CARBOHYD
 FT 478 478
 FT CARBOHYD
 FT 635 655
 FT VARSPLIC
 FT 635 655
 FT NALMK (in isoform C).
 FT FTId=VSP_002587.
 SQ SEQUENCE 761 AA; 83770 MW; F0CAD3252D7AB67E CRC64;
 Query Match 6.5%; Score 120; DB 1; Length 761;

Best Local Similarity 22.2%; Pred. No. 0.016;
 Matches 61; Conservative 40; Mismatches 114; Indels 60; Gaps 11;
 QY 31 NNSLMLOQSK-----ENHALASSSLCDEQIQONYSKVLAEYNTSPVGMATNAV 81
 Db 171 NNVIQIRIKKTDEGTYRCBGRILARGEI-----NFEDIVYVNPPTIARQNIY 221
 QY 82 LCPPIALRNLIITWEIILRGPSCTKAYAKETNETKNCUDERTITWSPDQNSDLQ 141
 Db 222 NATANLGGSVTLVCDAE---GPEPIMTSWTKD-GEQIEGDEDEKTYF---SDSSQLT 273
 QY 142 IRPVATHDGYRRICIMTTPDGNFRGHLYQVLYPPEVTLQNRK-----TAVCKAVA 194
 Db 274 IKKYDKDEAEVYIANKKAGEQDATIHLKFAKPKITYENQYAMELEQVTLTCEA-S 332
 QY 195 GKPAQISWIEPGDCATKQEWNSNGTVKSTCEWYHNVSTVY-----CHV 241
 Db 333 GDPISITWRSTNTNISSEKTLDGHVYVNSHA-----RVSLSLTKSIQYTDAGEYICTA 387
 QY 242 SHLGG--NKSXYITLLPVPKAKSKAKYIPYIILT 274
 Db 388 SNTIGQDSQSVTYLEVQYAP-----KIQGFVAVYT 416
 RESULT 9
 NCAL_HUMAN
 ID NCAL_HUMAN STANDARD; PRT; 848 AA.
 AC P13591; Q15829; Q16180;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neutral cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
 GN (NCAM-140) (CDS6 antigen).
 OS NCAM1 OR NCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=8075973;
 RX MEDLINE=94356433; Hayashi S., Kishimoto T., Kawase I.;
 RA Saito S., Taniro Y., Tachibana I.;
 RT "Complementary DNA sequence encoding the major neutral cell adhesion
 RT molecule isoform in a human small cell lung cancer cell line";
 RL Lung Cancer 10:307-318(1994).
 RN [2]
 RP SEQUENCE FROM N.A. PubMed=1710251;
 RX MEDLINE=91250739; PubMed=1710251;
 RA Lanier L.V., Chang C., Azuma M., Ruitenberg J.J., Hemperly J.J.,
 RA Phillips J.H.;
 RT "Molecular and functional analysis of human natural killer cell-
 RT associated neural cell adhesion molecule (N-CAM/CD56).";
 RL J. Immunol. 146:4421-4426(1991).
 RN [3]
 RP SEQUENCE OF 491-848 FROM N.A. PubMed=2887295;
 RX MEDLINE=87301755; PubMed=2887295;
 RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
 RA Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
 RT "Human muscle neural cell adhesion molecule (N-CAM): identification
 RT of a muscle-specific sequence in the extracellular domain";
 RL Cell 50:1119-1130(1987).
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
 CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
 CC neurites, etc.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=N-CAM 120;
 CC IsoId=P13591-1; Sequence=Displayed;
 CC Name=N-CAM 140;
 CC IsoId=P13592-2; Sequence=External;
 CC Name=C; Synonyms=Secreted;
 CC IsoId=P13592-1; Sequence=External;

CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD56 entry.
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd56.htm".
 CC -----
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 CC -----
 DR EMBL: S71824; AAB31836.1; -
 DR EMBL: U63041; AAB04558.1; -
 DR EMBL: M17410; AAB59913.1; -
 DR HSSP: P40189; IBOU.
 DR GeneW: HGNC:7656; NCAM1.
 DR MIM: 116930; -
 DR GO: GO:0016021; C: integral to membrane; TAS.
 DR GO: GO:0005886; C: plasma membrane; TAS.
 DR InterPro: IPR009857; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00408; IGC2; 5.
 DR PROSITE: PS50835; Ig_LIKE; 5.
 DR Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 DR Transmembrane; Alternative splicing.
 KM SIGNAL 1 19
 FT CHAIN 20 848
 FT TRANSMEM 709 708
 FT DOMAIN 730 848
 FT DOMAIN 20 111
 FT DOMAIN 116 205
 FT DOMAIN 212 301
 FT DOMAIN 308 403
 FT DOMAIN 406 491
 FT DOMAIN 518 595
 FT DOMAIN 660 727
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 287
 FT DISULFID 329 385
 FT DISULFID 426 479
 FT CARBOHYD 222 222
 FT CARBOHYD 315 315
 FT CARBOHYD 347 347
 FT CARBOHYD 423 423
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT CONFLICT 215 215
 FT CONFLICT 239 239
 FT CONFLICT 490 490
 FT CONFLICT 599 600
 FT CONFLICT 720 721
 FT CONFLICT 811 811
 SO SEQUENCE 848 AA; 93360 MW; 68D2F0C0E6C1C2AD CRC64;

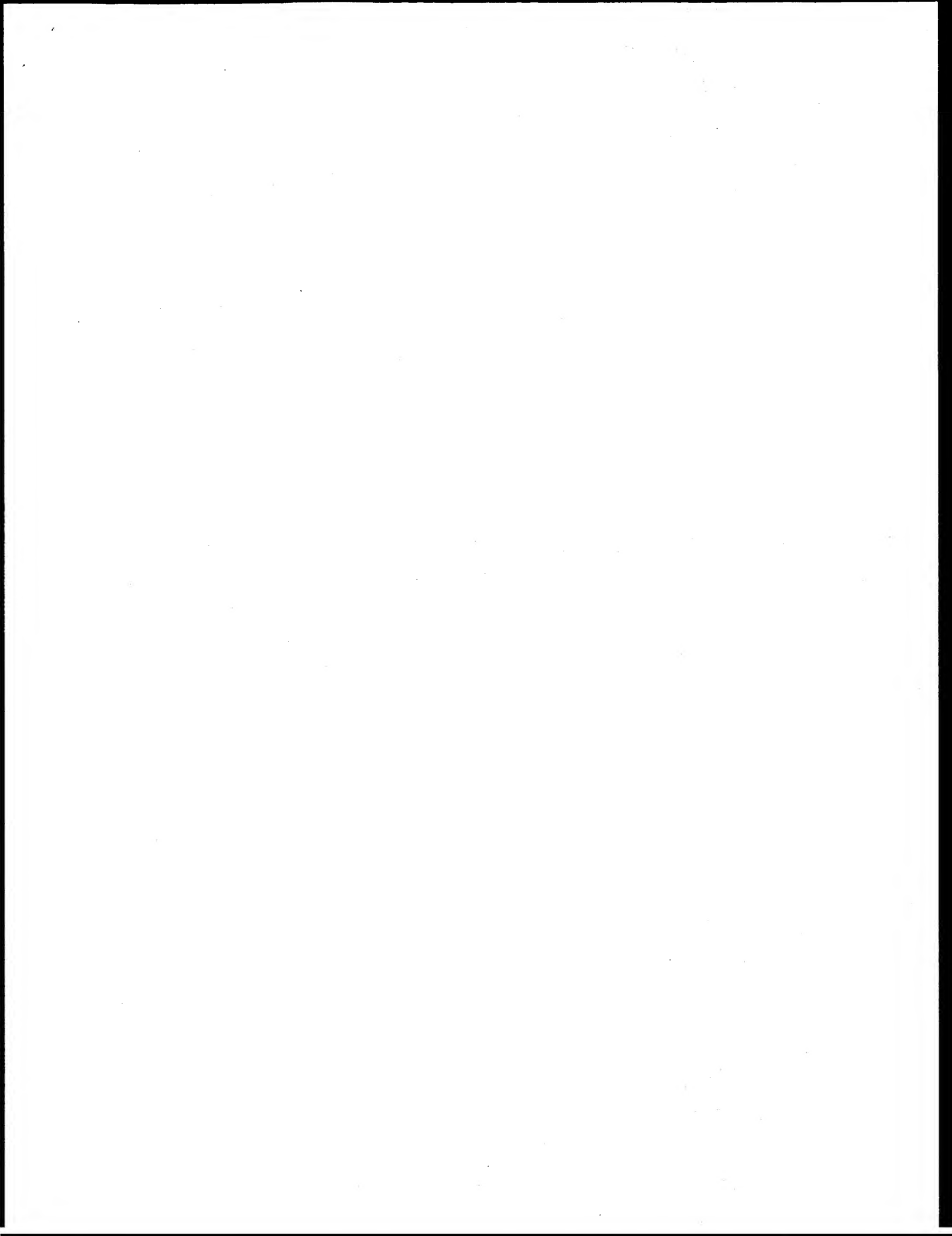
Query Match 6.5%; Score 120; DB 1; Length 848;
 Best Local Similarity 22.2%; Pred. No. 0.018;
 Matches 61; Conservative 40; Mismatches 114; Indels 60; Gaps 11;

QY 31 NNSLMLQTSK-----ENHALASSICMDEKQITQNSKVLAEVNTSPVQMAATNAV 81
 DB 171 NNYVLQIRGKKTDEGTGCEGRILARGEI-----NFDQIYIVVPTIQAQNIIV 221
 QY 82 LCCPIALNLIITWIIIRGQPSCTAYAKETNETKETCTDERITWVRPQNSDQ 141

DB 222 NATANIGSVTVLCAR-----GPEPTMSNTD-GEQIQEDDEKTYT-----SDSSQLT 273
 QY 142 IRPVATHDGYRCIMVTPDGFHRCYQLVTVTEVTLFQNR-----TAVCKAVA 194
 DB 274 IKVDKNDAAEYICIAENKAGQDATHLKVFAKPIYVENQTMELREQVTLNCEA-S 332
 QY 195 GKRAAISITPBGDCAKQEWNSNGVTKSCNHEVNVSTV-----CHV 241
 DB 333 GDIPISTWRTSTRNISSEKTLDGMMVRSNA-----RVSSLLKSIQYTDAGEYICRA 387
 QY 242 SHLTG-NKSLYIELLPVPAKKSANLYPIYILT 274
 DB 388 SNTIGDSQSMYLEVQYAP-----KLQSPVAVYT 416

RESULT 10
 CD86_RABIT STANDARD; PRT; 330 AA.
 ID CD86_RABIT
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen).
 GN CD86.
 OS Erytholagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NBL_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHB;HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T, Sato A;
 RT Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: Receptor involved in the costimulatory signal essential
 CC for T lymphocyte proliferation and interleukin 2 production, by
 CC binding CD28 or CTLA-4. May play a critical role in the early
 CC events of T cell activation and costimulation of naive T cells,
 CC such as deciding between immunity and anergy that is made by T
 CC cells within 24 hours after activation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D49842; AAB0642.1; -
 DR PIR: I46691; I46691.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KM Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KM Receptor.
 FT SIGNAL 1 22
 FT CHAIN 23 330
 FT TRANSMEM 23 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 330
 FT DOMAIN 33 127
 FT DOMAIN 150 225

POTENTIAL.
 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE V-TYPE.
 IG-LIKE C2-TYPE.



FT DISULFID 40 110 POTENTIAL.
 FT DISULFID 157 218 POTENTIAL.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 330 AA; 37142 MW; 935CD65C57E3EE1 CRC64;
 Query Match 6.5%; Score 119.5; DB 1; Length 330;
 Best Local Similarity 22.6%; Pred. No. 0.0663;
 Matches 77; Conservative 51; Mismatches 114; Indels 99; Gaps 18;
 14 LITTEFLVA-EAEGAAPNNISIMLOTSEKHNALASSLCMDKQITTONYSKYLAEVNTSW 72
 9 LSVTFVWALLISGA---SLRIQAYNKKA---DLPC---QPTNSQSRSLSLVFW 57
 73 PYKMATNAVLCPPPLALNLTITTEIIRGOPSCTKAKRETNETCTDEIITWS 132
 58 QDQER-----LVLEFLV-----GSEKEDNDPKIGTTS 87
 133 RPDQNSDLQIRPAVATHDGYRCIMWTPDGNFHRG-----YHLOVYLT---EV 178
 88 PPOESWNLQHLHVQIKDKKVOYCFV-----HHRGKGLVPIYQKNSLSVLANTOPEI 141
 179 TLFQNRRTA---VCKAVAGRP-AAQISWIEGDCATQOEWSNGYTVKSTCMWYHN 233
 142 TISNTIRNSAINTLCSSVQGYPEPKMFVKTENAT-TEX--GQVIEKSODNTGTLYN 198
 234 VS-----TWTCHVSHLTGNKSLYTELLPV---PQAKSAKJYIPYIILTI 275
 199 ISTSGSITSDIRNATITTCVLD--TESTETYSCHETIYPADPVEVPEKRLIAVALJTL 256
 276 IILT-IVGFIWLK-----VNGCRKYKLNKTESTPVE 307
 257 IYVGVIVLFTLMKRKKQOPGVCECETIKMDKAENEHVEE 297
 RESULT 11
 FAST_DROME STANDARD; PRT; 873 AA.
 ID FAS2_DROME AC P34082; P34083; Q9Y4M6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Fasciclin II precursor (FAS II).
 GN FAS2 OR EG:EG0007.3 OR CG3665.
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, SUBCELLULAR LOCATION,
 RP AND TISSUE SPECIFICITY.
 RC STRAIN=Canton-S;
 RC MEDLINE=2005695; PubMed=1913818;
 RA Greeningloh G., Rehm E.J., Goodman C.S.;
 RT "Genetic analysis of growth cone guidance in Drosophila: fasciclin II
 RT functions as a neuronal recognition molecule.";
 RL Cell 67:45-57(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agayuni A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delber A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Glaser K.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mentrlov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclebo J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassenaar D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertman B.P.,
 RA Bettencourt B.R., Celiker S.E., de Grey A.D.N.U., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.U., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RA "Annotation of the Drosophila melanogaster euchromatic genome: a
 RA systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [4]
 RP SEQUENCE OF 22-873 FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Galt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Borokova D.,
 RA Dreano S., Gloux S., Lelaire V., Mortier S., Galibert F., Borokova D.,
 RA Minana B., Katiatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papagiamakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
 RA Modolell J., Peter A., Schoettler P., Werner M., Mounkachi F.,
 RA Bellet N., Dowe G., Schaefer U., Jackle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamiou A., Henderson N.S.,
 RA McMillan P.J., Sallies C., Tait B.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RT melanogaster.";
 RL Science 287:2220-2222(2000).
 CC -1- FUNCTION: Neuronal recognition molecule for the MPI axon pathway,
 CC pathway recognition for axons during the development of nerve
 CC fascicles.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC attached to the membrane by a GPI-anchor (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing, Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1; Synonyms=A, Membrane-linked;

CC IsoId=P34082-1; Sequence=Displayed;
 CC Name=2; Synonyms=C; Phosphatidylinositol-linked;
 CC IsoId=P34082-2; Sequence=VSP_002508, VSP_002509;
 CC Name=3; Synonyms=B;
 CC IsoId=P34082-3; Sequence=VSP_002506, VSP_002507;
 CC -1- TISSUE SPECIFICITY: In embryos, both isoforms are initially
 CC expressed on the surface of the axons in the MPI pathway and later
 CC on several other longitudinal axon fascicles.
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 CC EMBL, M77165; AAA28527.1; -;
 CC EMBL, M77166; AAA28528.1; -;
 CC EMBL, AL033125; CAA21825.1; -;
 CC EMBL, AE003430; AAF45925.2; -;
 CC EMBL, AE003430; AAN09119.1; -;
 CC EMBL, AL033125; CAA21826.1; -;
 CC PIR, A41054; A41054;
 CC Flybase, FBgn000635; Fas2.
 CC GO, GO:0005886; C:Plasma membrane; IDA.
 CC GO, GO:0007156; P:homophilic cell adhesion; IDA.
 CC GO, GO:0007611; P:learning and/or memory; IMP.
 CC GO, GO:0016319; P:muscle body development; IMP.
 CC GO, GO:0008038; P:neural cell recognition; IDA.
 CC GO, GO:0054433; P:response to ethanol (sensu insecta); NAS.
 CC InterPro, IPR008557; FN_III-like.
 CC InterPro, IPR003961; FN_III.
 CC InterPro, IPR003598; IG_1-like.
 CC Pfam, PF00041; fn3; 2.
 CC Pfam, PF00047; ig; 5.
 CC SMART, SM00060; FN3; 2.
 CC SMART, SM00408; IG2; 3.
 CC PROSITE, PS00835; IG_LIKE; 5.
 CC Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
 CC Immunoglobulin domain; Transmembrane; GPI-anchor; Signal;
 CC Neurogenesis.
 CC KW SIGNAL
 CC CHAIN 1 28 POTENTIAL.
 CC DOMAIN 29 873 PASCTCLIN II.
 CC TRANSMEM 752 769 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 770 873 POTENTIAL.
 CC DOMAIN 31 131 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 138 223 IG-LIKE C2-TYPE 1.
 CC DOMAIN 230 318 IG-LIKE C2-TYPE 2.
 CC DOMAIN 323 423 IG-LIKE C2-TYPE 3.
 CC DOMAIN 428 520 IG-LIKE C2-TYPE 4.
 CC DOMAIN 544 619 FIBRONECTIN TYPE-III 1.
 CC DOMAIN 648 705 FIBRONECTIN TYPE-III 2.
 CC DISULFID 159 207 POTENTIAL.
 CC DISULFID 251 302 POTENTIAL.
 CC DISULFID 343 407 POTENTIAL.
 CC DISULFID 451 504 POTENTIAL.
 CC CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC VARSPLIC 737 773 GDIVGVAQVGVSSAAIVGAIAGVILLFVVDLDC ->
 CC DNPHTSGAPLAQLVIFTRLPMTLLILPPTHTA (in
 CC isoform 3).
 CC /FTId=VSP_002506.
 CC Missing (in isoform 3).
 CC VARSPLIC 774 873

FT VARSPLIC 738 811 /FTId=VSP_002507.
 FT IDTVARERQVPSAAIVGAIAGVILLFVVDLDCITV
 FT NGVATWCRKAKSPSEIDDAKGGGLVAP -> ESDS
 FT ANNMLGILLVAGNPSGVGALHRLFTTITLTAISTITL
 FT SITATTTITLTAISTITLTAISTITLTAISTITL (in isoform
 FT 2).
 FT /FTId=VSP_002508.
 FT VARSPLIC 812 873 Missing (in isoform 2).
 FT /FTId=VSP_002509.
 FT CONFLICT 804 804 S -> R (IN REF. 4; CAA21826).
 FT SQ SEQUENCE 873 AA, 96926 MW, E48F0484CCE62AC9 CRC64;
 Query Match 6.3%; Score 117; DB 1; Length 873;
 Best Local Similarity 22.5%; Pred. No. 0.03;
 Matches 69; Conservative 40; Mismatches 126; Indels 72; Gaps 14;
 QY 10 LGILLITL-----FLVAEAGAAQPNNSIMLOTSKENHALASSLCMDKQITQYYS 62
 DB 46 VKKPLILTRPVPVPPPSIVADLQMDNRRNTILPKNRGNOPMYETLPGSS----- 98
 QY 63 KYLAENVNMPVKA-----TNAYLCCEPIALRNLIITWEILRGG-PSCTKAYR 112
 DB 99 --LALMTISLSVWGCKYCTASANTLELKGVIKTYVALTTNNAPENQVFTIGQDYV 156
 QY 113 KETNETKENTCTDERITWVRPD-----QNSDLQRPVAITHDGYRC--INVT 159
 DB 157 VMCEVYADPNPT---IDMLRNGDPTRTNDKYVQTNGLLRNVQESDEGITCRAAVIE 213
 QY 160 PGNFRFGHLDQVLYTPV-----TLFQNNRRNVCVAVGKRAAOISWTEG---DC 209
 DB 214 TSELLERTTRIVAFQPELISLPTMLEAVGKPPALNCTA-RGKVPBELSWRDATQNV 272
 QY 210 ATKQEXWSN---GYTVKSTCHMEVNVSTVCHVSHLTG-----NKSILYIEL 254
 DB 273 ATKDRQVNPQGVLTIVSSVQ---DDYGTCTCLAKNRGVVDQKTLNVLVRPQY-EL 328
 QY 255 LPPGAK 261
 DB 329 YNVTGAR 335
 RESULT 12
 NCAL_CHICK STANDARD; PRT; 1091 AA.
 ID NCAL_CHICK
 AC P13590; G90918; G90919;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
 DE 180).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 1-175 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=67206150; PubMed=3576199;
 RA Cunningham B.A., Hemperly J.J., Murray B.A., Prediger E.A.,
 RA Brackenbury R., Edelman G.M.;
 RT "Neural cell adhesion molecule: structure, immunoglobulin-like
 RT domains, cell surface modulation, and alternative RNA splicing."
 RL Science 236:799-806 (1987).
 RN [2]
 RP SEQUENCE OF 128-1091 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=6206089; PubMed=3458261;
 RA Hemperly J.J., Murray B.A., Edelman G.M., Cunningham B.A.;
 RA "Sequence of a cDNA clone encoding the polysialic acid-rich and
 RT cytoplasmic domains of the neural cell adhesion molecule N-CAM."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3037-3041 (1986).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM D).
 RX MEDLINE=67092340; PubMed=3467341;

RA Hemperly J.J., Edelman G.M., Cunningham B.A.;
 RT "CDNA clones of the neural cell adhesion molecule (N-CAM) lacking a
 RT membrane-spanning region consistent with evidence for membrane
 RT attachment via a phosphatidylinositol intermediate.";
 RT Proc. Natl. Acad. Sci. U.S.A. 83:9822-9826(1986).
 RN [4]
 RP SEQUENCE OF 810-1069 FROM N.A.
 RX MEDLINE=87033934; PubMed=3771645;
 RA Murray B.A., Owens G.C., Prediger E.A., Crossin K.L.,
 RA Cunningham B.A., Edelman G.M.;
 RT "Cell surface modulation of the neural cell adhesion molecule
 RT resulting from alternative mRNA splicing in a tissue-specific
 RT developmental sequence.";
 RT J. Cell Biol. 103:1431-1439(1986).
 RN [5]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX MEDLINE=93122797; PubMed=1478668;
 RA Colwell G., Li B., Forrest D., Brackenbury R.;
 RT "Conserved regulatory elements in the promoter region of the N-CAM
 RT gene";
 RT Genomics 14:875-882(1992).
 RN [6]
 RP SEQUENCE OF 1-17 FROM N.A.
 RX STRAIN=White leghorn; TISSUE=Erythrocyte;
 RA Sasser M., Covault J.;
 RT Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
 CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
 CC neurites, etc.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A; Synonyms=N-CAM 180;
 CC IsoId=P13590-1; Sequence=Displayed;
 CC Name=B; Synonyms=N-CAM 140;
 CC IsoId=P13590-2; Sequence=VSP_002585;
 CC Name=C;
 CC IsoId=P13590-3; Sequence=VSP_002586;
 CC Name=D;
 CC IsoId=P13590-4; Sequence=VSP_002583; VSP_002584;
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----

DR EMBL; M15924; AAB59959.1; JOINED.
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 DR EMBL; M21180; AAB59958.1; JOINED.
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 DR EMBL; M15936; AAB59957.1; JOINED.
 DR EMBL; X04479; CAB51638.1; -
 DR EMBL; X70342; CAA4807.1; -
 DR EMBL; Z12128; CAA78113.1; -
 DR PIR; A43613; ICHNL.
 DR PDB; 1IE5; 08-AUG-01.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00041; FN3; 2.
 DR Pfam; PF00047; FN3; 5.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IGC2; 4.
 DR PROSITE; PS50835; IG LIKE; 5.
 DR Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KW Immunoglobulin domain; Alternating; Signal; 3D-structure.
 KM SIGNAL
 FT CHAIN 1 20 1091
 FT DOMAIN 20 721
 FT TRANSMEM 712 729
 FT DOMAIN 730 1091
 FT DOMAIN 20 113
 FT DOMAIN 116 205
 FT DOMAIN 212 301
 FT DOMAIN 308 403
 FT DOMAIN 406 495
 FT DOMAIN 518 595
 FT DOMAIN 624 692
 FT DOMAIN 152 156
 FT DOMAIN 161 165
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 287
 FT DISULFID 329 385
 FT DISULFID 426 479
 FT CARBOHYD 222 222
 FT CARBOHYD 315 315
 FT CARBOHYD 347 347
 FT CARBOHYD 423 423
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT VARSPLIC 702 726
 NEURAL CELL ADHESION MOLECULE 1, 180 KDA
 ISOFORM.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE C2-TYPE 1.
 IG-LIKE C2-TYPE 2.
 IG-LIKE C2-TYPE 3.
 IG-LIKE C2-TYPE 4.
 IG-LIKE C2-TYPE 5.
 FIBRONECTIN TYPE-III 1.
 FIBRONECTIN TYPE-III 2.
 HEPARIN-BINDING (POTENTIAL).
 HEPARIN-BINDING (POTENTIAL).
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 STPTSGTAAIVGIVTFVLL -> TLGSPSTSSSFV
 SLISAVLLILLC (in isoform D).
 /FTId=VSP_002583.


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FT  VARSPLIC  727  1091  Missing (in isoform D).
FT  VARSPLIC  771  809   Missing (in isoform B).
FT  VARSPLIC  810  1070  Missing (in isoform C).
FT  VARSPLIC  810  1070  Missing (in isoform C).
SQ  SEQUENCE  1091 AA; 117415 MW; B151367002DF8E80 CRC64;

Query Match 6.3%; Score 117; DB 1; Length 1091;
Best Local Similarity 22.6%; Pred. No. 0.044;
Matches 64; Conservative 39; Mismatches 104; Indels 76; Gaps 12;

Cy 31 NNSMLQTSK-----EKNHALASSSLCDEKQITON-----YSKYLAEVNTSMP 73
Db 171 NNYQIRKIKTDEGTVCGRILARGINIKDQVYVNPSPVARSQSTNATANISQS 230
Cy 74 VKAATNAVLCPPIALRNLIITWELIRGOPSCTKARKETNETKCTDERITVSR 133
Db 231 VTLACDADGFPPEP-----TWTV--TKDGEF-----TEQDNEKTSFNYD----- 268
Cy 134 PDQNSDIQIRPVATIHGVCRCIMWTDPGNFHRGYHLOVLTPEVTLFQNNR----- 186
Db 269 ---GSELTIKKVDSDENAFYICIAENKAGBODATIHLYVPAKPIYVKNKAMELEDQI 325
Cy 187 TAVCAVAGKAPPAQISWIPBGDCATKQRYWNGVTVKSTCHWEVHNVSTV----- 238
Db 326 TLTCGA-SGDPLPSITWKTSTRNISNEKTLDRIVASHA-----RVSSLTLEKIQYTD 379
Cy 229 -----CHVSHLTG--NKSLEYELFPVPAKSAKLYPIYILT 274
Db 380 AGEYVCTASNTIGDSQAMYLEVQYAP-----KIQGVAVAYT 416

RESULT 13
PR_HUMAN STANDARD; PRT; 417 AA.
ID PVR_HUMAN
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168426; PubMed=2538245;
RA Wendelschohn C.L.; Wimmer E.; Racanelli V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
RT sequence, and expression of a new member of the immunoglobulin
RT superfamily.";
RL Cell 56:855-865 (1989).
RN [2]
RP REVISIONS.
RA Racanelli V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S.; Horie H.; Ise I.; Okitsu A.; Yoshida M.; Iizuka N.;
RA Takeuchi K.; Takegami T.; Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
RT and secreted forms.";
RL EMBO J. 9:3217-3224 (1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyanagi V.; Severin J.; Ge Y.; Grable L.; Kvistad E.; Gordon L.;
RA Shannon M.; Brower A.; Olsen A.S.; Smith L.M.;
RT "Sequence analysis of a 1kb region in 19413.2 containing a zinc finger
RT gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

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DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0007125; F:invasive growth; TAS.
 DR InterPro; IPRO07110; IG-like.
 DR InterPro; IPRO03596; IG_v.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 Repeat; Antigen; Alternative splicing; Polymorphism.
 FT CHAIN 1 417
 FT SIGNAL 20
 FT DOMAIN 21 343
 FT TRANSMEM 344 367
 FT DOMAIN 368 417
 FT DOMAIN 24 139
 FT DOMAIN 145 237
 FT DOMAIN 244 338
 FT DISULFID 49 123
 FT DISULFID 166 221
 FT DISULFID 266 312
 FT CARBOHYD 105 105
 FT CARBOHYD 120 120
 FT CARBOHYD 188 188
 FT CARBOHYD 218 218
 FT CARBOHYD 237 237
 FT CARBOHYD 276 276
 FT CARBOHYD 307 307
 FT CARBOHYD 313 313
 FT VARSPLIC 340 384
 FT VARSPLIC 331 331
 FT VARSPLIC 332 384
 FT VARSPLIC 385 392
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 FT VARIANT 67 67
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 Query Match 6.3%; Score 115.5; DB 1; Length 417;
 Best Local Similarity 24.4%; Pred. No. 0.018; Mismatches 82; Indels 69; Gaps 11;
 Matches 59; Conservative 32; Mismatches 82; Indels 69; Gaps 11;
 QY 71 SWPVKATNAVLCPPIALRNLI-----TW 98
 DB 8 AMLLLVALLVLSWPPGTGVVQAPVPGVGLGDSVTLPCVLPVNNVTHVSLTW- 66
 QY 99 IIRGGPSCIKAKRKET-----NETKETCTDERITWSPDPNSLOIRPAVIRHGGV 153
 DB 67 --ARHSGSGMAVTHQTQGPVSSEKRLFAVARKLAEIR--NSLRHFGRLVDEGRY 121
 QY 154 RCIIMVT-PDGNFRGYHLYLTPE-----VTLFQNNKRTAVCKAVAGKPAQISWIP 205
 DB 122 TCFVTFPPQSRVDIMRLVLAEPQTAQVQLGGEVPMARCVSTGRPPAQITWHS 181
 QY 206 E--GDCAIKR-EVWSNGTIVKSTCMWEYHNS-----VYTGCHVSH-----LTGKS 249
 DB 182 DLQGMPTSGVPGFISGLTVLISL--WILVPSQVDGKNVTCVHESEPEKQLLVNLT 239
 QY 250 LY 251
 DB 240 VY 241

ID CAML_HUMAN STANDARD; RRT; 1257 AA.
 AC P32004; Q8TA87;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neural cell adhesion molecule LI precursor (N-CAM LI) (CD171 antigen).
 GN NCAM OR CAML1 OR MIC5.
 OS Homo sapiens (human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CC NCBI_TaxID=9606;
 RX MEDLINE=92031698; PubMed=1932117;
 RA Kobayashi M., Miura M., Asou H., Uyemura K.;
 RT "Molecular cloning of cell adhesion molecule LI from human nervous
 RT tissue: a comparison of the primary sequences of LI molecules of
 RT different origin";
 RL Biochim. Biophys. Acta 1090:238-240(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=92120663; PubMed=1769655;
 RA Hlaiv M.L., Lemmon V.;
 RT "Molecular structure and functional testing of human LICAM: an
 RT interspecies comparison";
 RL Genomics 11:416-423(1991).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92329299; PubMed=1627459;
 RA Reid R.A., Hemmery U.J.;
 RT "Variants of human LI cell adhesion molecule arise through alternate
 RT splicing of RNA";
 RL J. Mol. Neurosci. 3:127-135(1992).
 [4]
 RP SEQUENCE FROM N.A.
 RA Rosenthal A., Coutelle O., Drescher B.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97432815; PubMed=9286695;
 RA Brenner V., Nyakatura G., Rosenthal A., Platzner M.;
 RT "Genomic organization of two novel genes on human Xq28: compact head
 RT to head arrangement of IDH gamma and TRAP delta is conserved in rat
 RT and mouse";
 RL Genomics 44:8-14(1997).
 [6]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RX MEDLINE=98147998; PubMed=9479034;
 RA Coutelle O., Nyakatura G., Taudien S., Elgar G., Brenner S.,
 RA Platzner M., Drescher B., Joutel M., Kenwright S., Rosenthal A.;
 RT "The neural cell adhesion molecule LI: genomic organization and
 RT differential splicing is conserved between man and the pufferfish
 RT Fugu";
 RL Gene 208:7-15(1998).
 [7]
 RP SEQUENCE OF 20-36.
 RX MEDLINE=88298876; PubMed=3136168;
 RA Wolff J.M., Frank R., Mujoo K., Spiro R.C., Reisfeld R.A.,
 RA Rathjen F.G.;
 RT "A human brain glycoprotein related to the mouse cell adhesion
 RT molecule LI";
 RL J. Biol. Chem. 263:11943-11947(1988).
 [8]
 RP SEQUENCE OF 332-371 FROM N.A.
 RX MEDLINE=90353957; PubMed=2387585;
 RA Djebaili M., Watel M.-G., Nguyen C., Roux D., Demengeot J.,
 RA Denizot F., Moos X., Schachner M., Goriidis C., Jordan B.R.;
 RT "The gene encoding LI, a neural adhesion molecule of the
 RT immunoglobulin family, is located on the X chromosome in mouse and
 RT man";
 RL Genomics 7:587-593(1990).
 [9]

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RP SEQUENCE OF 353-1176 FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=92020233; PubMed=1923824;
RA Rosenblatt A., Mackinnon R.N., Jones D.S.C.;
RT "PCR walking from microdissection clone M54 identifies three exons
RT from the human gene for the neural cell adhesion molecule L1
RT (CAM-L1).";
RL Nucleic Acids Res. 19:5395-5401(1991).
RN [10]
RP SEQUENCE OF 809-1257 FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin F.B., Toshlycki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN [11]
RP SEQUENCE OF 1030-1257 FROM N.A.
RX MEDLINE=91132183; PubMed=1993895;
RA Harper J.R., Prince J.T., Healy P.A., Stuart J.K., Nauman S.J.,
RA Stralup W.B.;
RT "Isolation and sequence of partial cDNA clones of human L1: homology
RT of human and rodent L1 in the cytoplasmic region.";
RL J. Neurochem. 56:797-804(1991).
RN [12]
RP VARIANT HSAS TYR-264.
RX MEDLINE=94004956; PubMed=8401576;
RA Joutel M., Rozenblatt A., Macfarlane J., Kenwick S., Donnai D.;
RT "A missense mutation confirms the L1 defect in X-linked hydrocephalus
RT (HSAS).";
RL Nat. Genet. 4:331-331(1993).
RN [13]
RP VARIANT HSAS/MASA LEU-1194.
RX MEDLINE=95187172; PubMed=7681431;
RA Fransen E., Schrander-Stumpel C., Vits L., Coucke P., van Camp G.,
RA Willems P.J.;
RT "X-linked hydrocephalus and MASA syndrome present in one family are
RT due to a single missense mutation in exon 26 of the L1CAM gene.";
RL Hum. Mol. Genet. 3:2255-2256(1994).
RN [14]
RP VARIANT HSAS GLN-184 AND ARG-452, AND VARIANT MASA GLN-210.
RX MEDLINE=95004608; PubMed=7920659;
RA Joutel M., Rozenblatt A., Armstrong J., Macfarlane J., Stevenson R.,
RA Paterson J., Mettenberg A., Ionescu V., Temple K., Kenwick S.;
RT "X-linked spastic paraplegia (SPGL), MASA syndrome and X-linked
RT hydrocephalus result from mutations in the L1 gene.";
RL Nat. Genet. 7:402-407(1994).
RN [15]
RP VARIANT MASA GLN-210 AND ASN-598.
RX MEDLINE=95004609; PubMed=7920660;
RA Vits L., van Camp G., Coucke P., Fransen E., de Boule K.,
RA Reyniers E., Korn B., Poustka A., Wilson G., Schrander-Stumpel C.,
RA Winter R.M., Schwartz C., Willems P.J.;
RT "MASA syndrome is due to mutations in the neural cell adhesion gene
RT L1CAM.";
RL Nat. Genet. 7:408-413(1994).
RN [16]
RP VARIANT HSAS/MASA SER-9; SER-121; LYS-309; PHE-768; LEU-941 AND
RP CYS-1070.
RX MEDLINE=95282776; PubMed=7762552;
RA Joutel M., Moncla A., Paterson J., McKewon C., Fryer A., Carpenter N.,
RA Holmberg E., Madelin C., Kenwick S.,
RT "New domains of neural cell-adhesion molecule L1 implicated in
RT X-linked hydrocephalus and MASA syndrome.";
RL Am. J. Hum. Genet. 56:1304-1314(1995).
RN [17]
RP VARIANT HSAS/MASA GLN-184; GLN-210; TYR-264; ARG-452; ASN-598 AND
RP LEU-1194.
RX MEDLINE=96153146; PubMed=8556302;
RA Fransen E., Lemmon V., van Camp G., Vits L., Coucke P., Willems P.J.;
RT "CRASH syndrome: clinical spectrum of corpus callosum hypoplasia,
RT retardation, adducted thumbs, spastic paraparesis and hydrocephalus
RT due to mutations in one single gene, L1.";
RL Eur. J. Hum. Genet. 3:273-284(1995).
RN [18]
RP ERRATUM.
RA Fransen E., Lemmon V., van Camp G., Vits L., Coucke P., Willems P.J.;
RL Eur. J. Hum. Genet. 4:126-126(1996).
RN [19]
RP VARIANT HSAS/MASA/SPG1 SER-179 AND ARG-370.
RX MEDLINE=96057511; PubMed=7562969;
RA Ruiz J.C., Cuppens H., Legius E., Fryns J.-P., Glover T., Marynen P.,
RA Cassiman J.-J.,
RT "Mutations in L1-CAM in two families with X linked complicated
RT spastic paraplegia, MASA syndrome, and HSAS.";
RL J. Med. Genet. 32:549-552(1995).
RN [20]
RP VARIANT HSAS CYS-194 AND LEU-240.
RX MEDLINE=97083370; PubMed=8929944;
RA Gu S.-M., Orth U., Veske A., Enders H., Kluender K., Schloesser M.,
RA Engel W., Schwinger E., Gal A.,
RT "Five novel mutations in the L1CAM gene in families with X linked
RT hydrocephalus.";
RL J. Med. Genet. 33:103-106(1996).
RN [21]
RP VARIANT HSAS GLN-184; 439-VAL--THR-443 DEL; CYS-784 AND
RP 936-LEU--LEU-948 DEL.
RX MEDLINE=97338664; PubMed=9195224;
RA Macfarlane J.R., Du J.-S., Peyes M.E., Ramsden S., Donnai D.,
RA Charlton R., Garrett C., Tolmie J., Yates J.R.W., Berry C., Goudie D.,
RA Moncla A., Lunt P., Hodgson S., Joutel M., Kenwick S.;
RT "Nine novel L1 CAM mutations in families with X-linked
RT hydrocephalus.";
RL Hum. Mutat. 9:512-518(1997).
RN [22]
RP VARIANT HSAS/MASA ASP-691; ARG-698 AND PRO-935.
RX MEDLINE=98180721; PubMed=9521424;
RA Du Y.-Z., Srivastava A.K., Schwartz C.E.;
RT "Multiple exon screening using restriction endonuclease
RT fingerprinting (RPF): detection of six novel mutations in the L1 cell
RT adhesion molecule (L1CAM) gene.";
RN [23]
Query Match 6.2%; Score 115; DB 1; Length 1257;
Best local similarity 20.1%; Pred. No. 0.077;
Matches 64; Conservative 47; Mismatches 135; Indels 72; Gaps 11;

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Db 402 TOCEARNHSHLLANAYIVVQLPAKILTLADNOTNAVQSTAYLCKAFAPVSVQWL 461
 QY 287 LKVNCGCRKKKANKTESTPVEEDEMOPASTY-----EONPLXND 326
 Db 462 -----DEGGTVLQDERFFPYANGTLGIRDLQANDGRYFCLANDNNVTIM 509
 QY 327 TTNKVK-ASQALQSEVDT 343
 Db 510 ANLKKYKADATQITQGRST 527

RESULT 15
 NCAL RAT STANDARD, FRT, 858 AA.
 ID NCAL RAT P1356;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140) (NCAM-140).
 GN NCAM1 OR NCAM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88059265; PubMed=368385;
 RA Small S.J., Shull G.E., Sancon M.-J., Akeson R.;
 RT Identification of a cDNA clone that contains the complete coding
 sequence for a 140-kD rat NCAM polypeptide.;
 RL J. Cell Biol. 105:2335-2345(1987).
 [2]
 RP SEQUENCE OF 355-364 FROM N.A.
 RX MEDLINE=90166485; PubMed=2483093;
 RA Small S.J., Haines S.L., Akeson R.A.;
 RT Polypeptide variation in an N-CAM extracellular immunoglobulin-like
 fold is developmentally regulated through alternative splicing.;
 RL Neuron 1:1007-1017(1988).
 CC -1- FUNCTION: This protein is a cell adhesion molecule involved in
 neuron-neuron adhesion, neurite fasciculation, outgrowth of
 neurites, etc.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms are produced;
 CC Name=1;
 CC IsoId=P1356-1; Sequence=Displayed;
 CC -1- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; X06564; CAA29809.1; -;
 DR EMBL; M32611; AAA41679.1; -;
 DR PIR; S00846; IJRTNC.
 DR PDB; 1EPF; 27-OCT-00.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR007110; Ig_1-like.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00047; fn3; 2.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00408; IG2; 5.
 DR PROSITE; PS00835; IG_LIKE; 5.

KM Cell adhesion; Glycoprotein; Transmembrane; Repeat;
 KM Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
 KW 3D-structure.
 FT STGNL 1 19
 FT CHAIN 20 858
 FT
 FT DOMAIN 20 721
 FT TRANSEM 722 739
 FT DOMAIN 740 858
 FT DOMAIN 20 111
 FT DOMAIN 116 205
 FT DOMAIN 212 302
 FT DOMAIN 309 414
 FT DOMAIN 417 502
 FT DOMAIN 514 615
 FT DOMAIN 616 712
 FT DOMAIN 152 156
 FT DOMAIN 161 165
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 288
 FT DISULFID 330 396
 FT DISULFID 437 490
 FT CARBOHYD 222 222
 FT CARBOHYD 316 316
 FT CARBOHYD 348 348
 FT CARBOHYD 434 434
 FT CARBOHYD 460 460
 FT CARBOHYD 489 489
 SQ SEQUENCE 858 AA; 94658 MW; EAL0643E050E6 CRC64;

Query Match 6.2%; Score 114.5; DB 1; Length 858;
 Best Local Similarity 21.5%; Pred. No. 0.054;
 Matches 63; Conservative 39; Mismatches 106; Indels 85; Gaps 12;

QY 31 NNSLMTQSK-----ENHALASSLCMDKQTON-----YSKVLAEVNTSWP 73
 Db 171 NNYLQIRGIKKTDEGTGRCGRILARGEINFKIQIVVNPVYQARQSTVATATANGOS 230
 QY 74 VPKATNAVLCQPFALANLIIITWELLRQPSCTKAYRKETNETKETCTDERITWVR 133
 Db 231 VTLVCD-----DFFPEPTMSWTGDEPIENESEDEKHIP--- 266
 QY 134 PDQNSDIQIRPVALTHDGYRCIMWTPDGNFHRGYHQLQVTVPEVTLFQNRN----- 186
 Db 267 SDDSSELTIRVNDGNDAEAYCIENKAGQODASIHUKVAKPKETTYVENQTALEEQV 326
 QY 187 TAVGKAVAGKNAQISNIPESGDATKOE--YMS-----NGTVVKSCTCHWEVHNVT 236
 Db 327 TLVCEA-SGDPIPEITWRTSRNISSEKXSWTPPEKQETLDGHNVRSHA-----RVSS 380
 QY 237 VT-----CHVSHLTG--NKSLEYELLVPQAKKSAGATLYPIYLLT 274
 Db 381 LTLKSIQVTDAGEYITCTASNTIGQDSQSMYLEVYAP-----XLQSPVAVYT 427

Search completed: May 7, 2004, 11:41:13
 Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 11:36:39 ; Search time 45 Seconds
(without alignments)
2440.007 Million cell updates/sec

Title: US-10-009-445A-20

Perfect score: 1846
Sequence: 1 MLCWRTANLGLLILITFL.....NKVSAQALQSEVDTDLHTL 348

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.25.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_dactylap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	35.3	270	11	Q8BTP3
2	635	34.6	270	11	Q8BTP3
3	188	10.2	202	11	Q8BTP3
4	188	10.2	202	11	Q8BTP3
5	131	7.1	109	11	Q8BTP3
6	130.5	7.1	109	11	Q8BTP3
7	129	7.0	109	11	Q8BTP3
8	127.5	6.9	109	11	Q8BTP3
9	127	6.9	109	11	Q8BTP3
10	126	6.8	109	11	Q8BTP3
11	125.5	6.8	109	11	Q8BTP3
12	125.5	6.8	109	11	Q8BTP3
13	125.5	6.8	109	11	Q8BTP3
14	125	6.8	109	11	Q8BTP3
15	125	6.8	109	11	Q8BTP3
16	125	6.8	109	11	Q8BTP3

17	124	6.7	523	11	Q8K2H7
18	123.5	6.7	605	11	Q8K2H7
19	123.5	6.7	838	11	Q8C4B2
20	123.5	6.7	838	11	Q8C4B2
21	122.5	6.6	316	11	Q8BQ96
22	122	6.6	335	13	Q8BQ96
23	121	6.6	335	13	Q8BQ96
24	121	6.6	335	13	Q8BQ96
25	120.5	6.5	524	11	Q8K2H7
26	120	6.5	1093	4	Q8K2H7
27	119	6.4	858	4	Q8K2H7
28	118	6.4	1094	5	Q8K2H7
29	117	6.3	773	5	Q8K2H7
30	116.5	6.3	358	13	Q8K2H7
31	116.5	6.3	838	13	Q8K2H7
32	116	6.3	335	13	Q8K2H7
33	115.5	6.3	417	4	Q8K2H7
34	115.5	6.3	800	5	Q8K2H7
35	115.5	6.3	801	5	Q8K2H7
36	115.5	6.3	976	13	Q8K2H7
37	115.5	6.3	976	13	Q8K2H7
38	115	6.2	316	11	Q8K2H7
39	115	6.2	534	4	Q8K2H7
40	115	6.2	1255	4	Q8K2H7
41	114	6.2	534	6	Q8K2H7
42	114	6.2	846	13	Q8K2H7
43	114	6.2	1100	6	Q8K2H7
44	114	6.2	1255	6	Q8K2H7
45	113.5	6.1	1248	6	Q8K2H7

ALIGNMENTS

RESULT 1	Q8BTP3	PRELIMINARY	PRT	270 AA.
ID	Q8BTP3			
AC	Q8BTP3			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Similar to OX2 receptor.			
GN	F630003A1BR1K.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RE	SEQUENCE FROM N.A.			
RC	STRAIN=NOD;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium.			
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK089168; BAC0774.1;			
DR	MGI; MGI:2442797; F630003A1BR1K.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	SMART; SMO0409; IG; 1.			
DR	PROSITE; PS50835; IG; 2.			
DR	SEQUENCE 270 AA; 29528 MW; EFFIDBCDCECC317A CRC64;			
QY	Query Match	35.3%;	Score 651;	DB 11; Length 270;
QY	Best Local Similarity	48.8%;	Pred. No. 2.3e-53;	
QY	Matches 142; Conservative 33; Mismatches 86; Indels 30; Gaps 4;			
QY	6 RTANGLITLITLVAEAGAPNNISIMQTSKXHALASSLCMDKQITON-YSKV 64			
QY	6 RTPLTLTLITLITIV-			
QY	6 LAEVNTSWPVMATNAVLCPPIALRLIITWEIILRGDPSCTKAYRKEINTEKINCT 124			

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Db 40 LTVQVTTTSSVQIGTALACCFISIFLTKAVLITWIKMDLPSCTILYVDP-KITIEISCL 98
QY 125 DERITWVRSPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLTPEVTLFQNR 184
Db 99 DNNITWASTPDHSPBLQISAVTLQHEGYTCETVPEGNFGVYDLQVLTPEVTLFPGK 158
QY 185 NRTAVCKAVAGKPAQISWIPBGDCATQCEWNSGTWVTSCKHEWNVNSTVTCVSHL 244
Db 159 NRTAVCEAVAGKPAQISWIPBGDCVTTSESHSNGTIVRSTCHEWQNNVSAVSCVSHS 218
QY 245 TENKSLFIELNGSGSTTTTSLTILYKVVLLGILLHVGFAFPQKRVIR 269
Db 219 TENKSLFIELNGSGSTTTTSLTILYKVVLLGILLHVGFAFPQKRVIR 269

RESULT 2
ID Q8BTN8 PRELIMINARY; PRT; 270 AA.
AC Q8BTN8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to OX2 receptor.
F630003A18RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MOD;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The Riken Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK089193; BAC40786.1;
DR MGI; MGI:2442797; F630003A18RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_Like; 1.
SQ SEQUENCE 270 AA; 39581 MW; F381DBC62BF481F CRC64;

Query Match 34.6%; Score 639; DB 11; Length 270;
Best Local Similarity 48.5%; Pred. No. 3,1e-52;
Matches 141; Conservative 33; Mismatches 87; Indels 30; Gaps 4;

QY 6 RTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALASSSLCMEDEQITON-YEKV 64
Db 6 RTALTLILITFLVAEAGAAQPNNSIMLQTSKENHALASSSLCMEDEQITON-DSSSP 39
QY 65 LAEVNTSWPVKATNAVLCPPIALRNLIITWEIILRGQSPCTAYRKEINETYENCT 124
Db 40 LTVQVTTTSSVQIGTALACCFISIFLTKAVLITWIKMDLPSCTILYVDP-KITIEISCL 98
QY 125 DERITWVRSPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLTPEVTLFQNR 184
Db 99 DNNITWASTPDHSPBLQISAVTLQHEGYTCETVPEGNFGVYDLQVLTPEVTLFPGK 158
QY 185 NRTAVCKAVAGKPAQISWIPBGDCATQCEWNSGTWVTSCKHEWNVNSTVTCVSHL 244
Db 159 NRTAVCEAVAGKPAQISWIPBGDCVTTSESHSNGTIVRSTCHEWQNNVSAVSCVSHS 218
QY 245 TENKSLFIELNGSGSTTTTSLTILYKVVLLGILLHVGFAFPQKRVIR 269
Db 219 TENKSLFIELNGSGSTTTTSLTILYKVVLLGILLHVGFAFPQKRVIR 269

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RESULT 3
ID Q9D642 PRELIMINARY; PRT; 202 AA.
AC Q9D642;

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DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 4733401118RIK protein.
GN 483340919RIK OR 4733401118RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.U., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Holmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitlaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
RA Hayashizaki Y.;
RT Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
DR EMBL; AK014637; BAB29480.1;
DR MGI; MGI:1921853; 483340919RIK.
DR InterPro; IPR007110; IG-like.
SQ SEQUENCE 202 AA; 22804 MW; EAF3EBB70903A45B CRC64;

Query Match 10.2%; Score 188; DB 11; Length 202;
Best Local Similarity 27.4%; Pred. No. 1.3e-09;
Matches 55; Conservative 29; Mismatches 87; Indels 30; Gaps 4;

QY 6 RTANLGLLILITFLVAEAGAAQPNNSIMLQTSKENHALASSSLCMEDEQITONSKVL 65
Db 6 RTALMLLITFLTVPESSCVYKREI---PPDSFPSPDNIPPDGVGVTME----- 56
QY 66 AEVNTSWPVKATNAVLCPPIALRNLIITWEIILRGQSPCTAYRKEINETYENCT 125
Db 57 IEITPVSVQIGKQVLFCHPSPSKETLRIWITTPDWSCLPFAEIQISKLCTE 116
QY 126 ERITWVRSPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLTPEV----- 178
Db 117 RGTTRVRAHQSSDLPLKSMALKHGHYSRIETDQIFERSISIQVPGTISLPSLSTI 176
QY 179 -----TFQNFN 185
Db 177 LYVLAATVLLVGFAPQKRN 197

RESULT 4
ID Q9D628 PRELIMINARY; PRT; 205 AA.
AC Q9D628;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 483340819RIK protein.
GN 483340819RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Azakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Gissi C., Kling B., Kochina H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga M., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Rodriguez I., Sakamoto N.,
 RA Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK014671; BAB29497.1;
 DR MGI: MGI:1921853; 4833409J19Rik.
 DR InterPro: IPR007110; IG-like.
 SQ SEQUENCE 205 AA; 22874 MW; 7780C3DDC25B709 CRC64;

Query Match 10.2%; Score 188; DB 11; Length 205;
 Best Local Similarity 27.4%; Pred. No. 1.3e-09;
 Matches 55; Conservative 29; Mismatches 87; Indels 30; Gaps 4;
 QY 6 RTANGLILITLITFLVAEAGAAQPNNSIMLQTSKKNALASSLDCDEKQITONYSKVL 65
 DB 6 RTALMLILITLITLVPSSSCSVKREI---PPDPSPPDDIIPFDGVYME----- 56
 QY 66 AEVNTSVKMAVNAVLCPPALRNLIITWIIILGQSPCTAYRKETNETNCTD 125
 DB 57 IEITPVSQIGIKQKQFCHPSKEATRLIETTPRWPCRLPYAEALQOISKKICTE 116
 QY 126 ERIWVSPPDNQSDQIRPAVITHDGYRCIMVTPDGFHGHYGLVLPVEV----- 178
 DB 117 RGTTRVPAHQSSDPIKSMALKHGHSKRIETTDGIFGRHSIQVPGTISILPILSTI 176
 QY 179 -----TLFQNRN 185
 DB 177 LYVKLAIVTLVGFAPFQKRN 197

RESULT 5
 ID P70193 PRELIMINARY; PRT; 1091 AA.
 AC P70193;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Membrane glycoprotein.
 GN IRI1 OR IRI1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96394313; PubMed=8798419;
 RX Suzuki Y., Sato N., Toyama M., Wanka A., Takegi T.,
 RT "CDNA cloning of a novel membrane glycoprotein that is expressed
 RT specifically in glial cells in the mouse brain IRI-1: A protein with
 RT leucine-rich repeats and immunoglobulin-like domains";
 RL J. Biol. Chem. 271:22522-22527(1996).
 DR EMBL: D78572; BAAL1416.1; -
 DR PIR: A58532; A58532.
 DR HSSP; P56276; ITLK.

DR MGI: MGI:107935; IRI1.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_TYP.
 DR Pfam: PF00047; Ig; 3.
 DR Pfam: PF00560; LRR; 14.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF01462; LRRNT; 1.
 DR PRINTS: PR00019; LEUCRCHPT.
 DR SMART: SM00408; IGc2; 3.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00013; LRRNT; 1.
 DR SMART: SM00369; LRR_TYP; 4.
 DR PROSITE: PS00835; IG_LIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 1091 AA; 119283 MW; A13D0866CE4C203D CRC64;

Query Match 7.1%; Score 131; DB 11; Length 1091;
 Best Local Similarity 23.4%; Pred. No. 0.0029;
 Matches 64; Conservative 37; Mismatches 119; Indels 54; Gaps 14;
 QY 87 IALRNLIITWIIILGQSPCTAYRKETNETNCTD-----ERITVSPDNQSDQ 141
 DB 610 IAIKRTTARLCAATGHPNQAQKQGG-----IDFPAARBRMTV-WPDDIV-FF 660
 QY 142 IRPAVITHDGYRCIMVTPDGFHGHYGLVLPVEV-----EVLTFQNRN 187
 DB 661 ITDKKIDMGVYSCTRQNSAGSVANATITVLETSLAVPLEDRVTVGETVAFQ----- 715
 QY 188 AVCKAVAGKPAQGISWIPGD--CATKQWNSNGT--VTAKSCHEVAVNSTVTCVSH 243
 DB 716 --CKA-TGSPRTITLTKGRLSLTERHFTPGQQLVAVQVM--IDDAGRYCEMSN 769
 QY 244 LGNKSILY--IELPVPKAKSKAKLYPIIILITLITVGTITLTKVNGCRK---YKL 297
 DB 770 PLGTERAHSQSLILPFGCRKGTIVGITLAVGSIIVLISLVWCIIVQTKKSEBSYV 829
 QY 298 NKTESTPVVEDEMOFYASTEKNNPLVDTNKV 331
 DB 830 TNDDET-IVPDD---VPSYLSQGLSDRQETV 858

RESULT 6
 ID Q96RW7 PRELIMINARY; PRT; 5636 AA.
 AC Q96RW7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hemocentin.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Trent J.,
 RT "Human hemocentin gene";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF156100; AAK68690.1; -
 DR GO: GO:0005727; C:extrachromosomal circular DNA; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR000875; Cecropin.
 DR InterPro: IPR001434; DUF11.
 DR InterPro: IPR001881; EGF Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR009017; GFP_Like.

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003558; Ig_C2.
 DR InterPro: IPR000169; SH3Proc_acsite.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF00008; EGF_5.
 DR Pfam: PF00047; Ig_44.
 DR Pfam: PF00090; tsp_1; 6.
 DR SMART: SM00179; EGF_CA; 7.
 DR SMART: SM00408; IgC2; 43.
 DR SMART: SM00209; TSP1; 6.
 DR SMART: TIGR01451; B ant repeat; 9.
 DR TIGRFA: TIGR01451; B ant repeat; 9.
 DR PROSITE: PS00010; ASK HYDROXYL; 5.
 DR PROSITE: PS00268; CECROPIN; 1.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS01187; EGF_CA; 8.
 DR PROSITE: PS00835; IG_LIKE; 44.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
 DR PROSITE: PS50092; TSP1; 6.
 KM EGF-like domain; Immunoglobulin domain.
 SQ SEQUENCE 5636 AA; 613660 MW; F00B319CED7B52C CRC64;

Query Match 7.1%; Score 130.5; DB 4; Length 5636;
 Best Local Similarity 21.2%; Pred. No. 0.026;
 Matches 89; Conservative 55; Mismatches 142; Indels 133; Gaps 19;

QY 9 NLGLILITFLVAEAGAAOP-----NNSL-----MLQTSKENHAL 45
 DB 2396 NISVERKNSVSLCEASGIPLESTWFKDGPVSLNSVRLISGGRMLRMQITME---- 2451
 QY 46 ASSSLCMEDEKQITONTSKVLAENVNTPVYKATNAVLCPPIALRLIITTEILRGOP 105
 DB 2452 -----DAQGYTCVVRNNAAGEER-----KIFGLSVLPVPHVGENTL---EDVVKKEQ 2496
 QY 106 SCTKAVRKETNETKCTDERITW--VSRPDNSD-----LQIRPAITHDGY 153
 DB 2497 SVLTCEVTGNPPE-----ITMKDQPLQEDBAHIIISGGRLOITNVQVHTGRY 2549
 QY 154 RCIWTPDGNFHRGHLQVLYTP-----EVLFPQNRNTAVCAVAKPAQI 201
 DB 2550 TCLASSPAGHKSRFSFLNVSPTIAGVSDGNPDVTVILNPSLVECAVS--YPPAII 2608
 QY 202 SWIPEDCATKQYWGNGTIV-----KSTCHWEHNVSTYCHVSHLTGKSLYIEL 255
 DB 2609 TWKDG--TPLE--SKRNIRILPGRTLOILNAGDNAGRISCAVTAENAKIKAYEV- 2662
 QY 256 PVEGAKSAALYIPYIILITIIITIVGFIW-----LKYNG-----CRKYMLNKTE 301
 DB 2663 -----KVYIPPIINK-----GDLWGPGLSPREVKIKVNNLTLECAVYAI---P 2703
 QY 302 STEVVEDEMOFYASTEKKNPLDYTNKKYKASQ-----ALQGEVTDLLH 346
 DB 2704 SASLSWYKDGQPLKSDHVIANGHITLQKEAQISDTRGYTCVASNIAGEDELDPDV 2762

RESULT 7
 Q9ULB9 PRELIMINARY; PRT; 549 AA.

AC Q9ULB9
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Cell adhesion molecule nectin-3 alpha.
 GN PVR13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RX MEDLINE=20209403; PubMed=10744716;
 RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;
 RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
 RT that shows homophilic and heterophilic cell-cell adhesion
 RT activities.";
 RL J. Biol. Chem. 275:10291-10299 (2000).
 DR EMBL: AF195833; AAF63685.1; -.
 DR MGI: MGI:1930171; Pvr13.
 DR GO: GO:0005913; C:cell-cell adhesion junction; IDA.
 DR GO: GO:0005194; F:cell adhesion molecule activity; IDA.
 DR GO: GO:0005515; F:protein binding; IPT.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR003559; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00409; Ig_1.
 DR PROSITE: PS00835; IG_LIKE; 3.
 SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABBA72F185 CRC64;

Query Match 7.0%; Score 129; DB 11; Length 549;
 Best Local Similarity 20.2%; Pred. No. 0.0018;
 Matches 99; Conservative 44; Mismatches 136; Indels 210; Gaps 21;

QY 1 MLCFWRANIGLLITFLVAEAGAAOPNSIMLQTSKENHALASSLCMEDEKQIT-- 58
 DB 29 LILPAPTPPPLLLILFLSLCG-----ALAGSLIV--EPHYTAV 69
 QY 59 --QNYV--KVLAEVNTSPVKAATNAVLCPPIALRLIITTEILRGOPCTKARKET 115
 DB 70 WGRVSLKCLIEVN-----ETIQISWEKI--HGKSTQVAVAHHPQ 108
 QY 116 NETKETNCTDERITWVSRPDNSDLOIRPAITHDGYRCIMYT--PDGNFHRGHLQVLY 174
 DB 109 YGFSVQGDYQGRVLFKNYSIANDATITLMNIGFSDSGRTKAVTFPLGNAGSSTTVLV 168
 QY 175 TPBYTLFQ-----NKNRTAVCAVAKPAQISWIBEGD----- 208
 DB 169 EPTVSLIKGPDSLDGNENETVAACVATGKFAQIDW--EGDLGEMESSTSPNETAT 226
 QY 209 -----CATQO-----EY----- 215
 DB 227 IVSQYKLFPRFARGRRITCVVHPALEKDIRSFILIDIPABEVSTGYDGWFFVRKG 266
 QY 216 -----WSNGTYVASTCMEVH-----NVSTV--TCHVSHLTG 246
 DB 287 VNLKNADANPPRPKSVWSRLDQGPWDLASDVLTF--VHPLTVNYSGYVCKVSNLSG 345
 QY 247 NKS--LYTELFPV-----PG-----AKSAKLYIPYIIL-----TI 275
 DB 346 QRSQKVIYISDPTTTLQPTVQWSSPADVDIATEHKKLPPPLSTLATLKDDTIGTI 405
 QY 276 IITVGFIMLLKVN--GCRKYK-----LNKTESTPVEDEMOF 313
 DB 406 IASVVGALPLVLYVLSIAGVFCYRARRTFRGDYFAKNIYIPSPDQKESQIDVLHQDELDS 465
 QY 314 YASTEKNN 322
 DB 466 YPDSVKKEN 474

RESULT 8
 Q9ULB7 PRELIMINARY; PRT; 438 AA.

AC Q9ULB7
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Cell adhesion molecule nectin-3 gamma.
 GN PVR13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20209403; PubMed=10744716;
 RA Sacho-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
 RA Tachibana K., Mizoguchi A., Takai Y.,
 RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
 RT that shows homophilic and heterophilic cell-cell adhesion
 RT activities.";
 RL J. Biol. Chem. 275:10291-10299(2000).
 DR EMBL: AF195835; AAF63686.1; -.
 DR MGI: MGI:1930171; Pvr13.
 DR GO: GO:0005913; C:cell-cell adherens junction; IDA.
 DR GO: GO:0005194; F:protein binding; IPT.
 DR GO: GO:0005515; F:protein binding; IPT.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;
 SQ

Query Match 6.9%; Score 127.5; DB 11; Length 438;
 Best Local Similarity 21.3%; Pred. No. 0.0019;
 Matches 98; Conservative 44; Mismatches 136; Indels 183; Gaps 21;

QY 1 MLCPRNTANGLLITFLVAEAGAAQPNNSMLQTSKKNHALLASSLCMDKQIT-- 58
 DB 29 LLLPAPTPPPLLLPLPLLSRLCG-----ALAGSIIV--EPHVTAV 69
 QY 59 --QNVY-KYLAENVNSWPVKATNAVLCPPALANLIIITWEIILRGOPSCTKAYKET 115
 DB 70 WGNVSLKCLIEVN-----ETIQISWEKI-HGKSTQTVAAVHMQ 108
 QY 116 NETKETNCTDERITWVSRPDQNSDLQIRPVATTHDGYRCIMWT-PDGNFHHGYHLOLV 174
 DB 109 YGFSVQGYQGRVLEFNYSLNDATTTHNIGSDSKYICRAVTFPLGNAOSTTVTVLV 168
 QY 175 TPEVTLFQ-----NRRITAVCKAVAKPAQISWIPEDCATKOE--YWSNGVAT 208
 DB 169 EPTVSLIKGPDLLDGNFTVAACVAAATGKPAQIDW--EGDLGEMESSTTSFPMETAT 226
 QY 209 -----CATKQ-----EX----- 215
 DB 227 IVSYQYKLPPTPRFARGRITCVKHPALEKDIRVFIIDIQVAPESVTVGYDNFVGRKG 286
 QY 216 -----WSNGTVYKSTCHWEH-----NVSTV-TCHVSHLTG 246
 DB 287 VNLKCNADANPPPEKSVMSRLDQMPDGLASDNTLHF-VHPLTVNYSGVYVCKVSSSLG 345
 QY 247 NKS-----LYIELLP-----VPGAKSANKLYPIYLLITIIITVGFIVLTKVNGCRK 294
 DB 346 QRSDDKVIYISDIPLOTGSSIAVAGVGA-----VLALFITVFTV-TLPPRKKRP 397
 QY 295 YKLNKTESTPVEEDEMOPVASYTEK--NNPIYDTTNKYA 333
 DB 398 SYLDKVIDLPPTH---KPPVYERIRIPSLDKDLGQVRA 434

RESULT 9
 ID Q9JUB8 PRELIMINARY; PRT; 510 AA.
 AC Q9JUB8;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cell adhesion molecule nectin-3 beta.
 GN PVR13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20209403; PubMed=10744716;
 RA Sacho-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
 RA Tachibana K., Mizoguchi A., Takai Y.,
 RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
 RT that shows homophilic and heterophilic cell-cell adhesion
 RT activities.";
 RL J. Biol. Chem. 275:10291-10299(2000).
 DR EMBL: AF195834; AAF63686.1; -.
 DR MGI: MGI:1930171; Pvr13.
 DR GO: GO:0005913; C:cell-cell adherens junction; IDA.
 DR GO: GO:0005194; F:protein binding; IPT.
 DR GO: GO:0005515; F:protein binding; IPT.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR SEQUENCE 510 AA; 55811 MW; 45CE6E8F7454864 CRC64;
 SQ

Query Match 6.9%; Score 127; DB 11; Length 510;
 Best Local Similarity 24.2%; Pred. No. 0.0026;
 Matches 72; Conservative 36; Mismatches 114; Indels 76; Gaps 14;

QY 1 MLCPRNTANGLLITFLVAEAGAAQPNNSMLQTSKKNHALLASSLCMDKQIT-- 58
 DB 29 LLLPAPTPPPLLLPLPLLSRLCG-----ALAGSIIV--EPHVTAV 69
 QY 59 --QNVY-KYLAENVNSWPVKATNAVLCPPALANLIIITWEIILRGOPSCTKAYKET 115
 DB 70 WGNVSLKCLIEVN-----ETIQISWEKI-HGKSTQTVAAVHMQ 108
 QY 116 NETKETNCTDERITWVSRPDQNSDLQIRPVATTHDGYRCIMWT-PDGNFHHGYHLOLV 174
 DB 109 YGFSVQGYQGRVLEFNYSLNDATTTHNIGSDSKYICRAVTFPLGNAOSTTVTVLV 168
 QY 175 TPEVTLFQ-----NRRITAVCKAVAKPAQISWIPEDCATKOE--YWSNGVAT 222
 DB 169 EPTVSLIKGPDLLDGNFTVAACVAAATGKPAQIDW--EGDLGEMESSTTSFPMETAT 226
 QY 223 VKSTCHWEHVN-----SVTGVSHLTGKSL-YIELLPVQAKSANKLYPIYLLT 274
 DB 227 IVS--QYKLPPTPRFARGRITCVKHPALEKDIRVFIIDIQ-----YAPESVTV 274

RESULT 10
 ID Q9D006 PRELIMINARY; PRT; 549 AA.
 AC Q9D006;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE 2610301B19RIK protein.
 GN PVR13 OR 2610301B19RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arai K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Scuderi P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Guestinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nomberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wymshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayshtaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 DR EMBL; AK011949; BAB27933.1; -
 DR MGD; MGI:1930171; Pvr13.
 DR GO; GO:0005913; Cell-cell adhesion junction; IDA.
 DR GO; GO:0005194; F-cell adhesion molecule activity; IDA.
 DR GO; GO:0005515; F-protein binding; IPI.
 DR GO; GO:0007155; F-cell adhesion; IDA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00409; IG_1.
 DR PROSITE; PS50835; IG LIKE; 3.
 SQ SEQUENCE 549 AA; 60703 MW; 32775CBE67319B32 CRC64;

Query Match 6.8%; Score 126; DB 11; Length 549;
 Best Local Similarity 24.4%; Pred. No. 0.0035;
 Matches 73; Conservative 38; Mismatches 110; Indels 78; Gaps 15;

QY 1 MLCPTATLGLLITITFLVAGSAGAPNNLSIMQSKENHALASSLSCDEKQIT-- 58
 DB 29 LLLPAPPTPLLLPLPLLSRLG-----ALNGSLIV-EHVTAV 69
 QY 59 --QNTS-KYLAENVTSWPKVKAATNVLCCPPLALNLIITWELLKQPSCTKAYRET 115
 DB 70 WGNVSLKCLIEV-----ETITQISEKI-HGKSTQVAVHHPQ 108
 QY 116 NETKENCTDERITWVSRPDQNSDQIRPAITHHGYKCIWT-PDGNFHGYHQLVLT 174
 DB 109 YGFSVQDYGQVRLFNYSINDATITLHNIGFSDGSKYICKAVTPLLGAQSTTVLV 168
 QY 175 TREVTLFQ-----NENRTAVCKAVAKPAQISWIPBDCATKQY---WSNGTV 221
 DB 169 EPTVSLIKGPDSSIDGNETVAACVSTGKPAQIDW--EGDLG-EREFSTISPLNETA 225
 QY 222 TVKSTCHMEVHNV-----STVCHVSHLTGKNSL-YTELLPVPKAKKAKIYPIIILT 274
 DB 226 TVVS-QYELFPTFRARGRITCVHHPALEKDIRYSFTLDIQ-----YAEVSVT 274

RESULT 11

Q9UE16 PRELIMINARY; PRT; 449 AA.
 ID Q9UE16
 AC Q9UE16
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Polio virus related protein 2, alpha isoform (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA Yoshida K., Murray J.C.;
 RT "A transcriptional map in the region of 19q13 derived using direct
 sequencing and exon trapping";
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF044965; AAC82347.1; JOINED.
 DR EMBL; AF044962; AAC82347.1; JOINED.
 DR EMBL; AF044963; AAC82347.1; JOINED.
 DR EMBL; AF044964; AAC82347.1; JOINED.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG_2.

DR SMART; SM00409; IG_1
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 FT NON_TER 1
 SQ SEQUENCE 449 AA; 48152 MW; 6B0481EA70317CD2 CRC64;

Query Match 6.8%; Score 125.5; DB 4; Length 449;
 Best Local Similarity 24.7%; Pred. No. 0.0031;
 Matches 53; Conservative 32; Mismatches 87; Indels 43; Gaps 9;

QY 63 KYLAENVTSWPKVKAATNVLCC--PPLALNLIITWELLKQPSCTKAYR----- 112
 DB 7 QVLEVRG-----QLGTVELPCHLPLPVGILSVLTWQ-----RDPAPAHQNVAAFP 57
 QY 113 KETNETKCTDERITWVSRPD-----QNSDLQIRPAITHHGYKCIWT-PD 161
 DB 58 KMGPSPPSPKPSGERSLFSVANKSTGQDPAELQDATALHGLTVEDEGNYTCEFAFPK 117
 QY 162 GNFRHGYHQLVLT-----EYTLFQNRNRAVCAVAKPAQISWIPBDCATKQ 214
 DB 118 GSVRGMTWLVIAKPKNOAEQKVFESODPTVALCISKEGRPARISWLSIDWEAKET 177
 QY 215 YMSN---GTVTSTCHMEVHNV---TVTCHVSH 243
 DB 178 QVSGTLAIVTVTSRFTLVPSGRADGVTTCKYEH 212

RESULT 12

Q91VT9 PRELIMINARY; PRT; 467 AA.
 ID Q91VT9
 AC Q91VT9
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Similar to poliovirus sensitivity.
 GN PVRL2.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA Tissue-Breast tumor;
 RA Strauberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009088; AA09088.1; -
 DR MGD; MGI:97822; Pvr12.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_3.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS50835; IG LIKE; 3.
 SQ SEQUENCE 467 AA; 50756 MW; 6B00C4B70A018C1E CRC64;

Query Match 6.8%; Score 125.5; DB 11; Length 467;
 Best Local Similarity 26.2%; Pred. No. 0.0032;
 Matches 59; Conservative 37; Mismatches 82; Indels 47; Gaps 14;

QY 63 KYLAENVTSWPKVKAATNVLCC--PPLALNLIITWELLKQPSCTKAYRKE 114
 DB 37 RVLEVRG---RIGTVLEPCNLLPPTER-VSQVTWQRLDGVVAAFPBSEVDF--- 88
 QY 115 TNETKCTDERITWVSRPDQNSDQ-----IRPAITHHGYKCIWT-PDGNFHG 167
 DB 89 -----PNSGFSRDRISFPRARETNADLRDATALRGLRVEDGNYTCEFAFPNGTRGV 144
 QY 168 YHQLVLT-----EYTLFQNRNRAVCAVAKPAQISWIPBDCATKQY-S 217
 DB 145 TWLRVIAQPNHAEQVTTIGPQVAVARCVSTGGRPARITWSSIGAEKDTQEPGIG 204
 QY 218 NGVTVKSTCHMEVHNV-----TVTCHVSHLTGKNSLYTELLPV 257

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      ||| : |   ||| : : : |||
205 AGVTIIIS--RSLVPVGRADGVKNTCRVEHESFEEPI---LLPV 244
Db

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RESULT	13
08C6F2	
ID	08C6F2
PRELIMINARY	PRT
AA	467
AC	08C6F2
DT	01-MAR-2003 (TRENBLERel. 23, Created)
DT	01-MAR-2003 (TRENBLERel. 23, Last sequence update)
DT	01-OCT-2003 (TRENBLERel. 25, Last annotation update)
DE	Poliovirus sensitivity.
GN	PVR12.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxID=10090;

RESULT 14	
Q80XJ5	
ID_Q80XJ5	PRELIMINARY; PRT; 530 AA.
AC_Q80XJ5;	
DT 01-JUN-2003 (TrEMBLrel. 24, Created)	
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE Poliovirus receptor-related 2.	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.	
OX NCBI_TaxId=10090;	
NN [1]	

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stetlerion M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tshihyuli S., Carinini P., Prange C.,
RA Rata S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Joseph S.A., McMan P.J., McKernan K.J., Malek J.A., Gurrathne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heitton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzhanovskii M.I., Skalska U., Smalov D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
KL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RESULT 15		
ID	Q9V644	PRT; 433 AA.
AC	Q9V644;	PRELIMINARY;
DT	01-MAY-2000 (TrEMBLrel. 13)	(Created)
DT	01-MAY-2000 (TrEMBLrel. 13)	Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25)	Last annotation update)
DE	C89864 protein (KB41180p).	
GN	C89864.	
OS	Drosophila melanogaster (Fruit fly).	

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blasej R.G., Champs W., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrita U.F., Agayani A., An H.-C., Andrews-Plankoch C., Baldwin D.,
 RA Ballaw R.M., Sasu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodeson K., Doup E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Krafc C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Modyaty C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Maasman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agdayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dreenek D., Farian D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munco J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DDJ databases.
 DR EMBL: AEO03823; AAF58595.1; -;
 DR EMBL: AY089628; AAL90366.1; -;
 DR FlyBase: FBgn003674; CG8964.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; IG_3.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: PS00835; IG_LIKE; 3.
 DR Immunoglobulin domain;
 KM SEQUENCE 433 AA; 47700 MW; DF81DC747417D6B5 CRC64;
 SQ

Query Match 6.8%; Score 125; DB 5; Length 433;
 Best Local Similarity 21.7%; Pred. No. 0.0033;
 Matches 80; Conservative 55; Mismatches 142; Indels 92; Gaps 16;

Db 93 SEPQLEMTREDSRVALSKDSGALQFTSVLASDAGYQCOQLVIDSVASSSGVLLIVE 152
 QY 70 -----TSMPYKATNAVLCCPPIALRLNLLITWEILLRGQPSCTKAYRKETRET 121
 Db 153 QLFKVPQPTSKNLEGLTSKVHCK-----AGGTFAQVQVMKRETOLEPLV 197
 QY 122 NCTDERITWVSRPDQNSDLOIRPVAITHDGYTCIWTDPGNHRYHLCVLTPEVTLF 181
 Db 198 NVT-----DNGTLIFQVSNBQRQYTCIASNSQGITATVSVINVVAPKFSVP 247
 QY 182 QN-----RNRVAV--CKAVAGKPAQIOWIPE---GDCATKQEYMS---NGVTWKT 226
 Db 248 PEGPIVAAKGTAVIHQAL-GEKPTIQMDKLTLYINENTDPERFSLMENTL----- 301
 QY 227 CHMEVAVN-----STYCHVSLTGKSLYIELLPVPGAKSKAKLYPIYITITITIV 281
 Db 302 ---EIRVVRPEDEGRVYCTIGSSAGLKRETV-LLVTKSSKASNSVTRIIIVICLAF 357
 QY 282 GFTWLKVNCGCRKVK--LNKTE-----STPVEDEMOFYASYTEKNNPLYDTNKV 331
 Db 358 YFVLVGLTKVWYRRRLGKVLQEDGVNPGTQGHHDHNEBPCLTEANSS-KNLKSL 416
 QY 332 KASQALQSE 340
 Db 417 RESTITLEOE 425

Search completed: May 7, 2004, 11:42:12
 Job time : 48 secs

QY 28 ACPNNSLMTC-----TSKFNALASS-----LCMDKQITQNTYKTLAEVN 69